

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 00:33:44 ; Search time 1026.35 Seconds  
(without alignments)  
765.605 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27

Sequence: 1 aaacttcagtggtggacctccatgtt 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*

1: gb\_ba:\*\*

2: gb\_htg:\*\*

3: gb\_in:\*\*

4: gb\_om:\*\*

5: gb\_ov:\*\*

6: gb\_pat:\*\*

7: gb\_ph:\*\*

8: gb\_pl:\*\*

9: gb\_pr:\*\*

10: gb\_ro:\*\*

11: gb\_sts:\*\*

12: gb\_sy:\*\*

13: gb\_un:\*\*

14: gb\_vt:\*\*

15: em\_ba:\*\*

16: em\_fun:\*\*

17: em\_hum:\*\*

18: em\_in:\*\*

19: em\_mu:\*\*

20: em\_om:\*\*

21: em\_or:\*\*

22: em\_ov:\*\*

23: em\_pat:\*\*

24: em\_ph:\*\*

25: em\_pl:\*\*

26: em\_ro:\*\*

27: em\_sts:\*\*

28: em\_un:\*\*

29: em\_vt:\*\*

30: em\_htg\_hum:\*\*

31: em\_htg\_inv:\*\*

32: em\_htg\_other:\*\*

33: em\_htg\_mus:\*\*

34: em\_htg\_pln:\*\*

35: em\_htg\_rnd:\*\*

36: em\_htg\_mam:\*\*

37: em\_htg\_vrt:\*\*

38: em\_sy:\*\*

39: em\_htgo\_hum:\*\*

40: em\_htgo\_mus:\*\*

41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	100.0	27	6	AX281252
2	27	100.0	281	9	HSPSA4
3	27	100.0	711	6	AR153342
4	27	100.0	711	6	BD007601
5	27	100.0	870	9	HSA459783
6	27	100.0	876	9	HSA459782
7	27	100.0	990	9	HSU17040
8	27	100.0	992	6	I67863
9	27	100.0	1130	9	AF335477
10	27	100.0	1350	6	AX200986
11	27	100.0	1350	6	AX267642
12	27	100.0	1415	9	HUMPA4
13	27	100.0	1446	9	HUMAP5
14	27	100.0	1462	6	I67864
15	27	100.0	1466	6	E32812
16	27	100.0	1466	9	HSPSAR
17	27	100.0	1492	9	BC005307
18	27	100.0	1603	9	HSA310938
19	27	100.0	1654	9	HUMPA8
20	27	100.0	1729	6	AR059540
21	27	100.0	1729	6	AR082934
22	27	100.0	1729	6	AX337560
23	27	100.0	1729	9	HSPSA
24	27	100.0	1945	9	AF335478
25	27	100.0	2106	6	AX106218
26	27	100.0	3423	6	AX033404
27	27	100.0	3846	6	AX033402
28	27	100.0	4661	6	AX033400
29	27	100.0	4661	6	AX033401
30	27	100.0	5873	9	HSPSAG
31	27	100.0	6153	9	HUMPSANTIG
32	27	100.0	7130	6	A37262
33	27	100.0	7130	6	AR167395
34	27	100.0	7130	9	HUMPSAA
35	27	100.0	40458	2	AC011523
36	27	100.0	217346	2	AC027602
37	27	100.0	230000	9	AF243527
38	25.4	94.1	1514	9	MMPROS
39	21.2	78.5	146276	4	AC090889
40	21	77.8	569	9	S75755
41	21	77.8	708	9	HSA310937
42	20.6	76.3	95836	9	AC016710
43	20.6	76.3	146878	2	AC011174
44	20	74.1	20	6	I19503
45	20	74.1	20	6	I67851

ALIGNMENTS

RESULT 1	AX281252	AX281252	27 bp	DNA	linear	PAT 02-NOV-2001
LOCUS	Sequence 9 from Patent WO0176622.					
DEFINITION	AX281252					
ACCESSION	AX281252					
VERSION	AX281252.1	GI:16608508				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS	1					
TITLE						
JOURNAL						

synthetic construct.  
synthetic construct  
artificial sequences.

Pedyczak, A., Chong, P. and Sia, C.D.  
Immunogenic peptides derived from prostate-specific antigen (psa)  
and uses thereof  
Patent: WO 0176622-A 9 18-OCT-2001;

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FEATURES             Aventis Pasteur Limited (CA)
                      Location/Qualifiers
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QY 1 AAATTCAGTGTGGACCTCCATGTT 27
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Db 1 AAATTCAGTGTGGACCTCCATGTT 27
|||||

RESULT 2
HSPSA4               281 bp DNA linear PRI 24-FEB-1999
LOCUS                Human PSA gene for prostate specific antigen exon 4.
DEFINITION           X13943
ACCESSION            X13943
VERSION              1
KEYWORDS             kallikrein; prostate specific antigen; PSA gene.
SOURCE              Homo sapiens.
ORGANISM             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            1 (bases 1 to 281)
AUTHORS             Digby M.R.
TITLE               Direct Submission
JOURNAL             Submitted (09-JAN-1989) Digby M.R., The Howard Florey Institute,
                    Melbourne University, Parkville, Victoria 3052, Australia
REFERENCE            2 (bases 1 to 281)
AUTHORS             Digby M., Zhang X.Y. and Richards R.I.
TITLE               Human Prostate specific antigen (PSA) gene: structure and linkage
                    to the kallikrein-like gene, hK1-1
JOURNAL             Nucleic Acids Res. 17 (5), 2137 (1989)
MEDLINE             89183632
PUBMED              2467258
COMMENT              Data kindly reviewed (16-may-1989) by Digby M.R.
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                      /clone="CHK-2"
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                      <1..52
                      /number=3
                      <53..>189
                      /note="prostate specific antigen"
                      /codon_start=3
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                      /db_xref="GI:1335283"
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                      /translation="LTPKLCQVDLHVISNDVCAQVHPKVTKFMLCAGRTGKGKSTC
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RESULT 3
AR153342
LOCUS                Sequence 4 from patent US 6235486.
DEFINITION           AR153342
ACCESSION            AR153342
VERSION              1
KEYWORDS             AR153342.1 GI:15120874
SOURCE              Unknown.
ORGANISM             Unknown.
REFERENCE            1 (bases 1 to 711)
AUTHORS             Young C.Y.F., Tindall D.J. and Klee G.G.
TITLE               Method for detection of breast cancer
JOURNAL             Patent: US 6235486-A 4 22-MAY-2001;
FEATURES             Location/Qualifiers
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BASE COUNT          148 a 208 c 206 g 149 t
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Query Match          100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGGACCTCCATGTT 27
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Db 436 AAATTCAGTGTGGACCTCCATGTT 462
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RESULT 4
BD007601
LOCUS                711 bp DNA linear PAT 31-JAN-2002
DEFINITION           Method for detecting metastatic prostatic cancer.
ACCESSION            BD007601
VERSION              1
KEYWORDS             BD007601.1 GI:18635974
SOURCE              JP 2001503991-A/14.
ORGANISM             unidentified.
REFERENCE            1 (bases 1 to 711)
AUTHORS             Tindall,D.J., Young,C.Y.F., McCormic,D.J., Klee,G.G., Saedi,M.S.,
                    Kumar,A., Rittenhouse,H.G. and Wolfert,R.L.
TITLE               Method for detecting metastatic prostatic cancer
JOURNAL             Patent: JP 2001503991-A 14 27-MAR-2001;
COMMENT             MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH, HYBRITECH INC
                    OS Unidentified
                    PN JP 2001503991-A/14
                    PD 27-MAR-2001
                    PF 14-NOV-1997 JP 1998522888
                    PI 14-NOV-1996 US 08/759354
                    PI DONALD J TINDALL, CHARLES Y F YOUNG, DANIEL J MCCORMIC, PI
                    GEORGE G KLEE,
                    PI MOHAMMAD, SAEED SAEDI, ABHAY KUMAR, HARRY G RITTENHOUSE, PI
                    ROBERT L WOLFERT
                    PC C12N15/09,C07K16/40,C12N5/10,C12N9/64,C12P21/08,C12O1/68, PC
                    GOIN33/574,C12N15/00,C12N5/00
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                    CC Topology: Linear;
                    FH Key
                    FT source
                    FT Location/Qualifiers
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                      /organism="unidentified"
                      /db_xref="taxon:32644"
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Query Match          100.0%; Score 27; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.011;

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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTTCAGTGTGGACCTCCATGTT 27  
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 Db 436 AAACCTTCAGTGTGGACCTCCATGTT 462

RESULT 5  
 HSA459783  
 LOCUS  
 DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 2.  
 ACCESSION AJ459783  
 VERSION AJ459783.1 GI:20520642  
 KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Heuze-Vourc'h, N. and Courty, Y.  
 TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen)  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 870)  
 AUTHORS Courty, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabalais, 2 bis bvd Tonnelie, Tours, 37032 cedex, FRANCE  
 COMMENT alternative splice variant sequences: AJ459782, AJ459784.  
 FEATURES  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="YC140405-00"  
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 1..870  
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 CDS  
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 /note="alternative splice variant 2"  
 /codon\_start=1  
 /evidence=experimental  
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 /db\_xref="GI:20520643"  
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BASE COUNT 185 a 257 c 242 g 186 t  
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Query Match 100.0%; Score 27; DB 9; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTTCAGTGTGGACCTCCATGTT 27  
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 Db 529 AAACCTTCAGTGTGGACCTCCATGTT 555

RESULT 6  
 HSA459782  
 LOCUS  
 DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 1.

variant 1.  
 AJ459782  
 VERSION AJ459782.1 GI:20520640  
 KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Heuze-Vourc'h, N. and Courty, Y.  
 TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen)  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 876)  
 AUTHORS Courty, Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabalais, 2 bis bvd Tonnelie, Tours, 37032 cedex, FRANCE  
 COMMENT alternative splice variant sequences: AJ459783, AJ459784.  
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 Best Local Similarity 100.0%; Pred. No. 0.012;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTTCAGTGTGGACCTCCATGTT 27  
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 Db 406 AAACCTTCAGTGTGGACCTCCATGTT 432

RESULT 7  
 HSA17040  
 LOCUS  
 DEFINITION Human prostate specific antigen precursor mRNA, complete cds.  
 ACCESSION U17040  
 VERSION U17040.1 GI:595945  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

REFERENCE 1  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

in Benign and Malignant Prostate tissue  
Unpublished  
Moreno, J.M.  
Direct Submission  
Submitted (08-NOV-1994) Jose M J G Moreno, Urology, Thomas  
Jefferson University Hospital, 1025 Walnut Street, Philadelphia, PA  
19107, USA

Location/Qualifiers  
1. .990  
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209 a 291 c 273 g 217 t

BASE COUNT 209 a 291 c 273 g 217 t

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RESULT 8  
167863  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

I67863  
Sequence 13 from patent US 5674682.  
167863  
Unknown.  
Unclassified.  
Croch, C.; Gomeia, L.; Mulholland, S.; Grant, J.G. and  
Fisch, A.K.  
Nucleic acid primers for detecting micrometastasis of prostate  
cancer  
Patent: US 5674682-A 13 07-OCT-1997;  
Location/Qualifiers  
1. .990  
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210 a 291 c 272 g 217 t 2 others

Query Match 100.0%; Score 27; DB 6; Length 992;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
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RESULT 10  
AX200986  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AX200986  
Sequence 616 from Patent WO0151633.  
AX200986  
AX200986.1 GI:15390813  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1350)  
Xu, J.; Dillon, D.C.; Mitcham, J.L.; Harlocker, S.L.; Jiang, Y.;  
Reed, S.G.; Kalos, M.D.; Fanger, G.R.; Day, C.H.; Retter, M.W.;  
Stoik, J.A.; Skeiky, Y.A.; Wang, A. and Meagher, M.J.  
Comparisons and methods for the therapy and diagnosis of prostate  
cancer

RESULT 9  
AF335477  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF335477  
Homo sapiens prostate-specific antigen variant 1 mRNA, complete  
cdo, alternatively spliced.  
AF335477  
AF335477.1 GI:18478569  
Homo sapiens.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1130)  
David, A.; Majeesh, N.; Azar, I.; Biton, S.; Engel, S.; Bernstein, J.;  
Romano, J.; Avidor, Y.; Waks, T.; Eshhar, Z.; Langer, S.Z.;  
Lifshitz-Mercer, B.; Matzkin, H.; Rotman, G.; Toporik, A.; Savitsky, K.  
and Mintz, L.  
Unusual alternative splicing within the human kallikrein genes KLK2  
and KLK3 gives rise to novel prostate-specific proteins  
J. Biol. Chem. 277 (20), 18084-18090 (2002)  
11834722  
PUBMED  
22001285  
REFERENCE  
2 (bases 1 to 1130)  
David, A.; Engel, S.; Azar, I.; Bernstein, J.; Rotman, G.; Savitsky, K.  
and Mintz, L.  
Direct Submission  
Submitted (11-JAN-2001) Compugen Ltd., 72 Pinchas Rosen, Tel Aviv  
69512, Israel  
Location/Qualifiers  
1. .1130  
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ORIGIN

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AX200986  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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ORGANISM

AX200986  
Sequence 616 from Patent WO0151633.  
AX200986  
AX200986.1 GI:15390813  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1350)  
Xu, J.; Dillon, D.C.; Mitcham, J.L.; Harlocker, S.L.; Jiang, Y.;  
Reed, S.G.; Kalos, M.D.; Fanger, G.R.; Day, C.H.; Retter, M.W.;  
Stoik, J.A.; Skeiky, Y.A.; Wang, A. and Meagher, M.J.  
Comparisons and methods for the therapy and diagnosis of prostate  
cancer

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Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10  
AX200986  
LOCUS  
DEFINITION  
ACCESSION  
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AX200986  
Sequence 616 from Patent WO0151633.  
AX200986  
AX200986.1 GI:15390813  
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Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1350)  
Xu, J.; Dillon, D.C.; Mitcham, J.L.; Harlocker, S.L.; Jiang, Y.;  
Reed, S.G.; Kalos, M.D.; Fanger, G.R.; Day, C.H.; Retter, M.W.;  
Stoik, J.A.; Skeiky, Y.A.; Wang, A. and Meagher, M.J.  
Comparisons and methods for the therapy and diagnosis of prostate  
cancer

JOURNAL Patent: WO 0173032-A 616 19-JUL-2001;  
CORIXA CORPORATION (US)

FEATURES  
Source  
1. .1350  
/organism="Homo sapiens"  
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BASE COUNT 284 a 404 c 391 g 271 t  
ORIGIN

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QY 1 AAATTTCAGTGTGTGACCTCCATGTT 27  
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Db 1129 AAATTTCAGTGTGTGACCTCCATGTT 1155

RESULT 11  
AX267642  
LOCUS  
DEFINITION Sequence 616 from Patent WO0173032.  
ACCESSION AX267642  
VERSION AX267642.1 GI:16516315  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.  
and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer

JOURNAL Patent: WO 0173032-A 616 04-OCT-2001;  
CORIXA CORPORATION (US)

FEATURES  
source  
1. .1350  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
BASE COUNT 284 a 404 c 391 g 271 t  
ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTTCAGTGTGTGACCTCCATGTT 27  
|||||  
Db 1129 AAATTTCAGTGTGTGACCTCCATGTT 1155

RESULT 12  
HUMPAA  
LOCUS  
DEFINITION Human prostate specific antigen (PA) gene, 3 end, clone PA 75.  
ACCESSION M21895  
VERSION M21895.1 GI:189523  
KEYWORDS glycoprotein; prostate antigen; prostate-specific antigen;  
seminogelin.

SOURCE Human prostate tumor cell line PC 82, cDNA to mRNA, clone PA 75.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Riegman, P.H., Klaassen, P., van der Korput, J.A., Romijn, J.C. and  
Trapman, J.

TITLE Molecular cloning and characterization of novel prostate antigen  
cDNA's  
JOURNAL Biochem. Res. Commun. 155 (1), 181-188 (1988)  
MEDLINE 88326297

PUBMED 2458104  
FEATURES  
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1. .1415  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="19q13.3"  
1. .1415  
/gene="APS"  
1. .776  
/gene="APS"  
/note="prostate specific antigen precursor"  
/codon\_start=2  
/protein\_id="AAA59995.1"  
/db\_xref="GI:189524"  
/translation="VVFLLSVTWIGAAPLILSRVGVGWECEKHSQPMQVLVASRGRA  
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FLTPKKLQCVLDLHVISNDVCAQVHPKVKFMLCAGRWTKGKSTCGSGDGGPLVNGV  
LQGITTSWGSEPCALPSPSLYTKVHVYRWIKDTIVANP"  
1. .40  
/gene="APS"  
/note="prostate specific antigen signal peptide"  
62. .772  
/gene="APS"  
/product="prostate specific antigen"  
BASE COUNT 328 a 361 c 410 g 316 t  
ORIGIN 176 bp upstream of pvuII site.

sig\_peptide

mat\_peptide

Query Match 100.0%; Score 27; DB 9; Length 1415;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTTCAGTGTGTGACCTCCATGTT 27  
|||||  
Db 497 AAATTTCAGTGTGTGACCTCCATGTT 523

RESULT 13  
HUMAPS

LOCUS Homo sapiens prostate-specific antigen mRNA, complete cds.  
DEFINITION M26663  
ACCESSION M26663  
VERSION M26663.1 GI:618463  
KEYWORDS prostate-specific antigen.  
SOURCE Homo sapiens prostate gland cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Henttu, P. and Viikko, P.  
TITLE cDNA coding for the entire human prostate specific antigen shows  
high homologies to the human tissue kallikrein genes  
JOURNAL Biochem. Biophys. Res. Commun. 160 (2), 903-910 (1989)  
MEDLINE 89246551  
PUBMED 2470373  
COMMENT On Jan 5, 1995 this sequence version replaced gi:341511.  
Ref [1] reports bases 1..135 only.

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1. .1446  
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/db\_xref="taxon:9606"  
/map="19q13.3"  
/clone="PSA-20"  
/tissue\_type="prostate gland"  
1. .1446  
/gene="APS"  
1. .24  
/gene="APS"  
/note="G00-119-695"  
25. .810  
/gene="APS"  
/note="AA 18. .24 propeptide; AA 69 glycosylated Asn

residue"  
/codon\_start=1  
/product="prostate-specific antigen"  
/protein\_id="AA58802.1"  
/db\_xref="GI:618464"  
/db\_xref="GDB:G00-119-695"  
/translation="MWVPVFLTSLTWIGAAPLILSRIVGWCEKEHSQWQVLVAS  
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EPFELTKLQCDVLDHVISNDCAOVHPQKTKMLCAGRTGCKSTCGDSGGPLV  
CNGVLOGITSGSEPCALPERPSLYKVVHYRWKIDTIVNP"  
25...75

sig\_peptide

/gene="APS"  
/note="G00-119-695"

mat\_peptide

94...807  
/product="prostate-specific antigen"  
/note="G00-119-695"  
811...1446  
/gene="APS"  
/note="G00-119-695"

3'UTR

polyA\_site

1446  
/gene="APS"  
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333 a 372 c 419 g 322 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 1446;  
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27  
|||||  
Db 532 AAATTCAGTGTGTGGACCTCCATGTT 558

RESULT 14

I67864

LOCUS 167864 1462 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 14 from patent US 5674682.  
ACCESSION 167864  
VERSION 167864.1 GI:2829986  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1462)

Croce, C., Gomella, L., Mulholland, S. Grant., Moreno, J. G. and  
Fischer, R.  
Nucleic acid primers for detecting micrometastasis of prostate  
cancer

JOURNAL Patent: US 5674682-A 14 07-OCT-1997;  
FEATURES Location/Qualifiers

1..1462  
/organism="unknown"  
BASE COUNT 343 a 374 c 422 g 323 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27  
|||||  
Db 532 AAATTCAGTGTGTGGACCTCCATGTT 558

RESULT 15

E32812

LOCUS 1466 bp RNA linear PAT 31-JAN-2002  
DEFINITION Primer DNA and method for detecting mRNA encoding prostate  
gland-specific antigen by using the same.  
E32812

E32812.1 GI:18623942  
JP 2000069969-A/5.  
unidentified.  
SOURCE unidentified.  
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1466)

AUTHORS Nakagawa, H.  
TITLE Primer DNA and method for detecting mRNA encoding prostate  
gland-specific antigen by using the same  
Patent: JP 2000069969-A 5 07-MAR-2000;

JOURNAL HITACHI CHEMICAL CO LTD, KK NIHON IDENSHI KENKYUJO

COMMENT OS Unidentified

PN JP 2000069969-A/5

PD 07-MAR-2000

PF 28-AUG-1998 JP 1998243419

PR HIRAKAZU NAKAGAWARA

PC C12N15/09, C12Q1/68, C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Key Location/Qualifiers

FT source 1..1466

FT /organism="Unidentified".

FT Location/Qualifiers

1..1466

/organism="Unidentified".

/db\_xref="taxon:32644"

BASE COUNT 338 a 382 c 422 g 324 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27

|||||

Db 551 AAATTCAGTGTGTGGACCTCCATGTT 577

Search completed: November 19, 2002, 04:02:55

Job time : 1028.68 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 ; Search time 1542.46 Seconds  
(without alignments)  
283.494 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27

Sequence: 1 aacttcagtggtggacctccatgtt 27

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	189	9	AA657663 nt82c06.s
2	27	100.0	196	12	BF58362 RC5-FT019
3	27	100.0	239	12	BF58359 RC5-FT019
4	27	100.0	241	12	BE76940 PM1-FT002
5	27	100.0	272	14	T29518 EST82635 Hu
6	27	100.0	288	12	BF588848 7112c03.x

310	9	AA522842	AA522842 nt172c08.s
319	12	BF56613	BF56613 MR1-FT020
328	9	AA654296	AA654296 nt83c06.s
329	12	BF58271	BF58271 RC5-FT019
351	12	BE38775	BE38775 RC6-FN011
354	12	BE771925	BE771925 CM3-FT009
373	9	AA228953	AA228953 nc14a04.f
388	9	AA228822	AA228822 nc15a04.s
398	9	AA635287	AA635287 nt17b07.s
400	12	BF476990	BF476990 na58all.
406	9	AA420570	AA420570 nc61b06.f
420	9	AA228836	AA228836 nc16h06.f
426	9	AA226359	AA226359 nc17h09.f
429	12	BF56615	BF56615 MR1-FT020
429	12	BF56642	BF56642 MR1-FT020
436	9	AA630877	AA630877 nt58a05.s
439	9	AA569482	AA569482 nt23a11.s
453	9	AA573727	AA573727 nt43e09.s
454	12	BE769339	BE769339 PM2-FT002
457	9	AI926979	AI926979 wg68d11.x
466	9	AA654527	AA654527 nt59a12.s
471	9	AA654924	AA654924 nt77e07.s
481	9	AA579159	AA579159 nt28b08.s
489	9	AA658261	AA658261 nu21c03.s
491	9	AA225115	AA225115 nc21g11.s
505	9	AA574023	AA574023 nt44f11.s
514	9	AI989309	AI989309 38 protsta
520	9	AA534235	AA534235 nj70e05.s
520	12	BF56617	BF56617 MR1-FT020
540	12	BF56640	BF56640 MR1-FT020
542	9	AA654548	AA654548 nt59d11.s
554	9	AA579039	AA579039 nt34g07.s
582	9	AA594946	AA594946 nc04c01.s
591	12	BF679591	BF679591 602154033
636	12	BF678378	BF678378 602085809
681	9	AI732097	AI732097 nc21g11.x
724	12	BF964653	BF964653 602267731
732	9	AI547309	AI547309 PN001_AH
738	12	BF679168	BF679168 602153741

#### ALIGNMENTS

RESULT 1  
AA657663 189 bp mRNA linear EST 05-NOV-1997  
LOCUS nt82c06.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1205002  
DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN).  
mRNA sequence.  
AA657663  
AA657663.1 GI:2593817  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 189)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.  
Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	189	9	AA657663 nt82c06.s
2	27	100.0	196	12	BF58362 RC5-FT019
3	27	100.0	239	12	BF58359 RC5-FT019
4	27	100.0	241	12	BE76940 PM1-FT002
5	27	100.0	272	14	T29518 EST82635 Hu
6	27	100.0	288	12	BF588848 7112c03.x

Trace considered overall poor quality  
Seq primer: -40ml3 fwd ET from Amerisham  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

source

1. .189  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1205002"  
/clone\_lib="NCI\_CGAP\_P3"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"  
/note="Vector: pAMP10; Site.1: NotI; Site.2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected cells histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (life technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

## BASE COUNT

43 a 44 c 54 g 48 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 189;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAATTCAGTGTGTGGACCTCCATGTT 27  
Db 10 AAATTCAGTGTGTGGACCTCCATGTT 36

## RESULT 2

BF858362 196 bp mRNA linear EST 16-JAN-2001  
LOCUS RC5-FT0193-211100-012-G09\_1 FT0193 Homo sapiens cDNA, mRNA  
DEFINITION  
ACCESSION BF858362  
VERSION BF858362.1 GI:12246106  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 196)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## MEDLINE

20202663

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2707001  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-211100-012-G09\_1&t3=2000-11-21&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 190.  
Location/Qualifiers

## FEATURES

Location/Qualifiers

source

1. .196  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="FT0193"  
/dev\_stage="Adult"

/note="Organ: prostate\_tumor; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

41 a 58 c 55 g 42 t

## BASE COUNT

ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 196;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAATTCAGTGTGTGGACCTCCATGTT 27  
Db 146 AAATTCAGTGTGTGGACCTCCATGTT 172

## RESULT 3

BF858359/c 239 bp mRNA linear EST 16-JAN-2001  
LOCUS RC5-FT0193-211100-012-G07 FT0193 Homo sapiens cDNA, mRNA sequence.  
DEFINITION  
ACCESSION BF858359  
VERSION BF858359.1 GI:12246103  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 239)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

## JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## MEDLINE

20202663

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-FT0193-211100-012-G07&t3=2000-11-21&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 239.  
Location/Qualifiers

## FEATURES

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1. .239  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="FT0193"  
/dev\_stage="Adult"

/note="Organ: prostate\_tumor; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."



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BASE COUNT      52 a      67 c      70 g      50 t
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
|||||
Db 94 AAATTCAGTGTGTGGACCTCCATGTT 68

RESULT 4
LOCUS      BE769440
DEFINITION PM1-FT0028-030700-001-c02_1 FT0028 Homo sapiens cDNA, mRNA
ACCESSION  BE769440
VERSION     BE769440.1 GI:10223098
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 241)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
,M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ft2-pm1-FT0028-030
700-001-c02_1&t3=2000-07-03&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 241.
FEATURES
source
1..241
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FT0028"
/dev_stage="Adult"
/notes="Organ: prostate tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      51 a      71 c      68 g      51 t
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
|||||
Db 146 AAATTCAGTGTGTGGACCTCCATGTT 172

us-09-829-004a-9.rst
BASE COUNT      52 a      67 c      70 g      50 t
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
|||||
Db 94 AAATTCAGTGTGTGGACCTCCATGTT 68

RESULT 5
LOCUS      T29518
DEFINITION T29518 Human Prostate gland Homo sapiens cDNA 5' end similar to
antigen, prostate specific (HT:2350), mRNA sequence.
ACCESSION  T29518
VERSION     T29518.1 GI:611616
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 272)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
,C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
,O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A.,
Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald
,L.M., FitzHugh, W.M., Fritchman, J.L., Geoghagen, N.S.M., Glodek, A.,
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.P.S., Kelley, J.M.,
Klimek, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J.,
Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-W.,
Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L.,
Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei
,Y.F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon
,M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
Venter, J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)
96026280
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
FEATURES
source
1..272
/organism="Homo sapiens"
/db_xref="ATCC (inhost):106527"
/cl_xref="taxon:9606"
/clone_lib="Human Prostate gland"
/notes="Organ: prostate gland"
BASE COUNT      62 a      81 c      71 g      56 t      2 others
ORIGIN
Query Match      100.0%; Score 27; DB 14; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
|||||
Db 190 AAATTCAGTGTGTGGACCTCCATGTT 216

RESULT 6
LOCUS      BF588848/c
DEFINITION 7112c03.x1 NCI CGAP Br16 Homo sapiens cDNA clone IMAGE:3334468 3'
similar to SW:PROS_HUMAN P07288 PROSTATE SPECIFIC ANTIGEN PRECURSOR
,, mRNA sequence.
ACCESSION  BF588848
VERSION     BF588848.1 GI:11681172
KEYWORDS   EST.

```

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 288)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@remail.nih.gov  
Tissue Procurement: Dennis Sgroi, M.D., Kristina Cole, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov  
Seq primer: -40RP from Gibco.  
Location/Qualifiers  
1..288  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3334468"  
/clone\_lib="NCI-CGAP\_Br16"  
/sex="female"  
/tissue\_type="lobular carcinoma in situ"  
/dev\_stage="adult"  
/lab\_host="DH103"  
/note="Organ: breast; Vector: PAMP1; mRNA made from breast  
carcinoma tissue, cDNA made by oligo-dr priming.  
Directionally cloned. Size-selected on agarose gel,  
average insert size 400 bp. Primary library,  
non-amplified."  
59 a 83 c 87 g 59 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 288;  
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;  
Matches 27; Conservative 0

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27  
Db 119 AAACCTCAGTGTGGACCTCCATGTT 93

RESULT 7  
AA522842/c  
LOCUS  
DEFINITION  
ni72c08.s1 NCI-CGAP\_Prl2 Homo sapiens cDNA clone IMAGE:982382  
similar to gp:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN).  
mRNA sequence.  
AA522842  
VERSION  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@remail.nih.gov  
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,  
Rodrigo F. Chuquai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 426 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham.  
Location/Qualifiers  
1..310  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:982382"  
/clone\_lib="NCI-CGAP\_Prl2"  
/sex="male"  
/tissue\_type="Metastatic prostate bone lesion"  
/lab\_host="DH103"  
/note="Vector: PAMP10; mRNA made from metastatic prostate  
lesion of the bone, cDNA made by oligo-dr priming.  
Non-directionally cloned. Size-selected on agarose gel,  
average insert size 600 bp. Library made by D. Krizman,  
NIH."  
72 a 82 c 62 g 94 t

BASE COUNT  
ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 310;  
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;  
Matches 27; Conservative 0

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27  
Db 302 AAACCTCAGTGTGGACCTCCATGTT 276

RESULT 8  
BF856613/c  
LOCUS  
DEFINITION  
MFL1561200-311000-001-b11 FT0200 Homo sapiens cDNA, mRNA sequence.  
BF856613  
VERSION  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Dias Neto, E., Garcia  
Nagai, M.A., da Silva  
Goldman, G.H., Carvalheira, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=HRI&t2=MFL-FT0200-  
311000-001-b11&t3=2000-10-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 269.  
Location/Qualifiers  
1..319  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="FT0200"  
/dev\_stage="Adult"  
/note="Organ: prostate\_tumor; Vector: puc18; Site: 1; SmaI;

Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.

BASE COUNT 64 a 84 c 95 g 76 t  
ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 319;

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27

|||||  
Db 66 AAACCTCAGTGTGGACCTCCATGTT 40

RESULT 9

AA654296

LOCUS

DEFINITION

AA654296 328 bp mRNA linear EST 04-NOV-1997  
nt83c06 s1 NCI-CGAP Pr3 Homo sapiens cDNA clone IMAGE:1205098  
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN  
); contains MSRI.b2 MSRI repetitive element 1, mRNA sequence.

ACCESSION

AA654296

VERSION

AA654296.1

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 328)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

, Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

DNA sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.

Clone distribution: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40m13 fwd. Et from Amersham

High quality sequence stop: 298.

Location/Qualifiers

1..328

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1205098"

/clone\_lib="NCI-CGAP\_Pr3"

/sex="Male"

/dev\_stage="45 years old"

/lab\_host="DH10B"

/notes="Vector: pAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st

strand cDNA was primed with oligo(dT)17 on 50 ng of

DNase-treated, total cellular RNA obtained from 5,000-10

,000 microdissected cells histologically-determined to be

fully malignant prostate cancer cells. Double-stranded

cDNA was ligated to EcoRI adaptors, 5 cycles of PCR

applied to the cDNA with an adaptor-specific primer, and

the resulting PCR product subcloned into pAMP10 by the

UDG-cloning method (Life technologies). Average insert

size is 600 bp. NOTE: Not directionally cloned. This

library was constructed by David Krizman."

BASE COUNT 66 a 76 c 113 g 73 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27

|||||

Db 150 AAACCTCAGTGTGGACCTCCATGTT 176

|||||

RESULT 10

BF858271/c

LOCUS

DEFINITION

RC5-FT0193-201100-012-H06 FT0193 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BF858271

VERSION

BF858271.1

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 329)

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC56t2-RC5-FT0193-

201100-012-H06&t3=2000-11-20&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 48.

High quality sequence stop: 329.

Location/Qualifiers

1..329

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="FT0193"

/dev\_stage="Adult"

/note="Organ: prostate tumor; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 68 a 99 c 96 g 66 t

ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 329;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27

|||||

Db 184 AAACCTCAGTGTGGACCTCCATGTT 158

|||||

RESULT 11

BE838775

LOCUS

DEFINITION

RC6-FN0114-090800-011-F04 FN0114 Homo sapiens cDNA, mRNA sequence.

Query Match 100.0%; Score 27; DB 9; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.19;



found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -28m13 rev1 ET from Amersham  
High quality sequence stop: 342.

## FEATURES

source

1. .373  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:1008078"  
/clone\_lib="NCI\_CGAP\_Pr1"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"

/note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 78 a 106 c 107 g 82 t

## ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 373;

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27

Db 203 AACTTCAGTGTGTGGACCTCCATGTT 229

## RESULT 14

AA228822/c

## LOCUS

DEFINITION AA228822 388 bp mRNA linear EST 20-AUG-1997  
nc15a04.s1 NCI\_CGAP\_Pr1 Homo sapiens cDNA clone IMAGE:1008174  
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);

RNA sequence.

ACCESSION AA228822.1 GI:1851679

VERSION AA228822.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 388)

NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

, Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 648 Std Error: 0.00

Seq primer: -4lm13 fwd. ET from Amersham

High quality sequence stop: 341.

## FEATURES

source

1. .388

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:1008174"

/clone\_lib="NCI\_CGAP\_Pr1"

/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"

/note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into PAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT 81 a 119 c 102 g 86 t

## ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 388;

Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGTGGACCTCCATGTT 27

Db 314 AACTTCAGTGTGTGGACCTCCATGTT 288

## RESULT 15

AA635287

## LOCUS

DEFINITION AA635287 398 bp mRNA linear EST 03-DEC-1997  
nt71b07.s1 NCI\_CGAP\_Pr3 Homo sapiens cDNA clone IMAGE:1203925  
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);

RNA sequence.

ACCESSION AA635287.1 GI:2619092

VERSION AA635287.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 398)

NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Nov 12, 1997 this sequence version replaced gi:2559129.

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

, Michael Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert length: 651 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

## FEATURES

source

1. .398

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:1203925"

/clone\_lib="NCI\_CGAP\_Pr3"

/sex="Male"

/dev\_stage="45 years old"

/lab\_host="DH10B"

/note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st

strand cDNA was primed with oligo(dT)17 on 50 ng of

DNase-treated, total cellular RNA obtained from 5,000-10,

000 microdissected cells histologically-determined to be

fully malignant prostate cancer cells. Double-stranded

cDNA was ligated to EcoRI adaptors, 5 cycles of PCR

applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

BASE COUNT  
ORIGIN

88 a 106 c 116 g 88 t

Query Match 100.0%; Score 27; DB 9; Length 398;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGTCAGTGTGTGACCTCCATGTT 27  
Db 118 AAAGTCAGTGTGTGACCTCCATGTT 144

Search completed: November 19, 2002, 05:17:33  
Job time : 1545.46 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:04:51 ; Search time 91.3846 Seconds  
(without alignments)  
111.898 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27

Sequence: 1 aaacttcagtggtgacccatggtt 27

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 33578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*

11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*

13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	100.0	27	10	US-09-829-004A-9
2	27	100.0	1350	10	US-09-759-143-616
3	27	100.0	1350	10	US-09-780-669-616
4	27	100.0	1350	10	US-09-822-827-616
5	27	100.0	1729	10	US-09-969-708-598
6	27	100.0	1758	10	US-09-822-827-977
7	27	100.0	2406	10	US-09-822-827-980
8	27	100.0	3423	10	US-09-755-100-5
9	27	100.0	3846	10	US-09-755-100-3
10	27	100.0	4661	10	US-09-755-100-1
11	27	100.0	4661	10	US-09-755-100-2
12	19.6	72.6	461	10	US-09-969-708-280
13	19.6	72.6	601	10	US-09-919-580-72
14	19.6	72.6	684	10	US-09-919-580-34
15	19.6	72.6	1168	10	US-09-925-300-603
16	18.8	69.6	792	10	US-09-770-445-844
17	18.8	69.6	2181	9	US-09-938-8428-1866
18	18.2	67.4	1678	10	US-09-925-300-133
19	18.2	67.4	2417	10	US-09-759-143-334

20	18.2	67.4	2417	10	US-09-780-669-334	Sequence 334, App
21	18.2	67.4	2417	10	US-09-822-827-334	Sequence 334, App
22	18.2	67.4	3674	10	US-09-759-143-698	Sequence 698, App
23	18.2	67.4	3674	10	US-09-780-669-698	Sequence 698, App
24	18.2	67.4	3674	10	US-09-822-827-698	Sequence 698, App
25	18.2	67.4	202001	10	US-09-734-674-3	Sequence 3578, App
c 26	18	66.7	453	10	US-09-974-300-3578	Sequence 3578, App
c 27	18	66.7	3360	9	US-09-954-531-1379	Sequence 1379, App
c 28	18	66.7	3360	9	US-09-954-531-1379	Sequence 1379, App
c 29	17.4	64.4	365	10	US-09-960-352-2463	Sequence 2463, App
c 30	17.4	64.4	407	10	US-09-960-352-13191	Sequence 13191, App
c 31	17.4	64.4	16552	10	US-09-764-855-321	Sequence 321, App
c 32	17.4	64.4	16552	10	US-09-764-855-322	Sequence 322, App
c 33	17.2	63.7	305	10	US-09-880-107-899	Sequence 899, App
c 34	17.2	63.7	575	10	US-09-864-761-12568	Sequence 12568, App
c 35	17.2	63.7	861	10	US-09-925-297-286	Sequence 286, App
c 36	17.2	63.7	871	10	US-09-962-832-101	Sequence 101, App
c 37	17.2	63.7	871	10	US-09-880-107-2307	Sequence 2307, App
c 38	17	63.0	2652	12	US-10-041-395-6	Sequence 6, Appl1
c 39	17	63.0	2997	12	US-10-041-395-4	Sequence 4, Appl1
c 40	17	63.0	3531	12	US-10-041-395-3	Sequence 3, Appl1
c 41	17	63.0	3878	12	US-10-041-395-1	Sequence 1, Appl1
c 42	17	63.0	10378	10	US-09-764-847-1938	Sequence 1938, App
c 43	16.6	61.5	417	10	US-09-878-571-2142	Sequence 2142, App
c 44	16.6	61.5	1235	10	US-09-764-869-2083	Sequence 2083, App
c 45	16.6	61.5	1235	10	US-09-764-869-2084	Sequence 2084, App

ALIGNMENTS

RESULT 1

US-09-829-004A-9

Sequence 9, Application US/09829004A

Patent No. US20020132976A1

GENERAL INFORMATION:

APPLICANT: Chong, Pele

APPLICANT: Pedyczak, Artur

APPLICANT: Sia, Charles Dwo Yuan

TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Antigen (P

TITLE OF INVENTION: Uses Thereof

FILE REFERENCE: 11014-24

CURRENT APPLICATION NUMBER: US/09/829,004A

CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: US 60/195,456

PRIOR FILING DATE: 2000-04-10

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.0

SEQ ID NO 9

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: CLP316

US-09-829-004A-9

Query Match 100.0%; Score 27; DB 10; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.00059;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGGACCTCCATGTT 27  
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Db 1 AAACCTCAGTGTGTGGACCTCCATGTT 27

RESULT 2

US-09-759-143-616

Sequence 616, Application US/09759143

Patent No. US20020022248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqui  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, William  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT APPLICATION NUMBER: US/09/759,143  
CURRENT FILING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 1350  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-759-143-616

Query Match 100.0%; Score 27; DB 10; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGTCAGTCGTGGACCTCCATGTT 27  
|||||  
DB 1129 AAAGTCAGTCGTGGACCTCCATGTT 1155

RESULT 3  
US-09-780-669-616  
Sequence 616, Application US/09780669  
Patent No. US20020051977A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqui  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C24  
CURRENT APPLICATION NUMBER: US/09/780,669  
CURRENT FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 1350  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-780-669-616

Query Match 100.0%; Score 27; DB 10; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGTCAGTCGTGGACCTCCATGTT 27  
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DB 1129 AAAGTCAGTCGTGGACCTCCATGTT 1155

RESULT 4  
US-09-822-827-616  
Sequence 616, Application US/09822827  
Patent No. US20020081680A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.534C1  
CURRENT APPLICATION NUMBER: US/09/822,827  
CURRENT FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 982  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 1350  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-822-827-616

Query Match 100.0%; Score 27; DB 10; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 0.0013;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGTCAGTCGTGGACCTCCATGTT 27  
|||||  
DB 1129 AAAGTCAGTCGTGGACCTCCATGTT 1155

RESULT 5  
US-09-969-708-598  
Sequence 598, Application US/09969708  
Patent No. US20020102532A1  
GENERAL INFORMATION:  
APPLICANT: Augustus, Meena  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
FILE REFERENCE: 689250-70  
CURRENT APPLICATION NUMBER: US/09/969,708  
CURRENT FILING DATE: 2001-10-03  
PRIOR APPLICATION NUMBER: US/60/237,606  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US/60/237,608  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: US/60/237,425  
PRIOR FILING DATE: 2000-10-03  
NUMBER OF SEQ ID NOS: 658  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 598  
LENGTH: 1729  
TYPE: DNA  
ORGANISM: Homosapiens  
US-09-969-708-598

Query Match 100.0%; Score 27; DB 10; Length 1729;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGTCAGTCGTGGACCTCCATGTT 27  
|||||  
DB 813 AAAGTCAGTCGTGGACCTCCATGTT 839

RESULT 6



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US-09-822-827-977
; Sequence 977, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 977
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-977

Query Match      100.0%; Score 27; DB 10; Length 1758;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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Db 1537 AAACCTCAGTGTGGACCTCCATGTT 1563

RESULT 7
US-09-822-827-980
; Sequence 980, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 980
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-980

Query Match      100.0%; Score 27; DB 10; Length 2406;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
   ||||||||||||||||||||||||||||
Db 1129 AAACCTCAGTGTGGACCTCCATGTT 1155

RESULT 8
US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1
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; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match      100.0%; Score 27; DB 10; Length 3423;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
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Db 2009 AAACCTCAGTGTGGACCTCCATGTT 2035

RESULT 9
US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

Query Match      100.0%; Score 27; DB 10; Length 3846;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCTCCATGTT 27
   ||||||||||||||||||||||||||||
Db 2432 AAACCTCAGTGTGGACCTCCATGTT 2458

RESULT 10
US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match      100.0%; Score 27; DB 10; Length 4661;
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Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
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Db 3247 AAATTCAGTGTGTGGACCTCCATGTT 3273

RESULT 11
US-09-755-100-2
; Sequence 2, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-2

Query Match 100.0%; Score 27; DB 10; Length 4661;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTCAGTGTGTGGACCTCCATGTT 27
    ||||| ||||| ||||| ||||| |||||
Db 3247 AAATTCAGTGTGTGGACCTCCATGTT 3273

RESULT 12
US-09-969-708-280/c
; Sequence 280, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-708-280

Query Match 72.6%; Score 19.6; DB 10; Length 461;
Best Local Similarity 84.6%; Pred. No. 3.3;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAATTCAGTGTGTGGACCTCCATGTT 27
    ||||| ||||| ||||| ||||| |||||
Db 178 AAATTCATGTTGGACCTGCATATT 153
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RESULT 13
US-09-919-580-72/c
; Sequence 72, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-580-72

Query Match 72.6%; Score 19.6; DB 10; Length 601;
Best Local Similarity 84.6%; Pred. No. 3.5;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGGACCTCCATGTT 27
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Db 187 AACTTCATGTTTGGACCTGCATATT 162

RESULT 14
US-09-919-580-34/c
; Sequence 34, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 89, 92, 122, 123, 295, 320, 322, 352, 355, 361, 369, 375,
; LOCATION: 382, 384, 386, 389, 409, 411, 413, 414, 415, 421, 440, 445,
; LOCATION: 448, 453, 461, 500, 510, 538, 532, 537, 546, 547, 563, 564,
; LOCATION: 569, 577, 583, 587, 597, 598, 599, 609, 613, 616, 621
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc.feature
; LOCATION: 622, 627, 648, 681
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-34

Query Match 72.6%; Score 19.6; DB 10; Length 684;
Best Local Similarity 84.6%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTTCAGTGTGTGGACCTCCATGTT 27
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Db 198 AACTTCATGTTTGGACCTGCATATT 173

RESULT 15
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US-09-925-300-603
; Sequence 603, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 603
; LENGTH: 1168
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1121)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1122)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1133)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1153)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-603

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Query Match      72.6%; Score 19.6; DB 10; Length 1168;
Best Local Similarity 84.6%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY      2  AACTTCAGTGTGGACCTCCATGTT 27
Db      931  AACTTCATGTTGGACCTCATATT 956

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OM nucleic - nucleic search, using sw model

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(without alignments)  
765.605 Million cell updates/sec

Title: US-09-829-004A-7

Perfect score: 24  
Sequence: 1 atgtgggtcccggtgtgtcttcttc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	6	AX281250	Sequence
2	24	100.0	70	6	AR147236	Sequence
3	24	100.0	389	9	HSPSA1	Human PSA g
4	24	100.0	569	9	S75755	PSA-prostat
5	24	100.0	708	9	HS310937	Sequence
6	24	100.0	870	9	HS310937	Sequence
7	24	100.0	876	9	HS310937	Sequence
8	24	100.0	990	9	HS310937	Sequence
9	24	100.0	992	6	HS310937	Sequence
10	24	100.0	1095	9	HS310937	Sequence
11	24	100.0	1130	9	AF335477	Sequence
12	24	100.0	1446	9	HUMAPS	Sequence
13	24	100.0	1462	6	E32812	Sequence
14	24	100.0	1466	6	E32812	Sequence
15	24	100.0	1466	9	HSPSAR	Sequence
16	24	100.0	1492	9	EC005307	Sequence
17	24	100.0	1603	9	HS310938	Sequence
18	24	100.0	1709	6	AX033403	Sequence
19	24	100.0	1795	9	AF335478	Sequence
20	24	100.0	2106	6	AX106218	Sequence
21	24	100.0	3423	6	AX033404	Sequence
22	24	100.0	3846	6	AX033402	Sequence
23	24	100.0	4661	6	AX033400	Sequence
24	24	100.0	4661	6	AX033401	Sequence
25	24	100.0	5873	9	HSPSAG	Sequence
26	24	100.0	6153	9	HUMPSANTIG	Sequence
27	24	100.0	7130	6	A37262	Sequence
28	24	100.0	7130	6	AR167395	Sequence
29	24	100.0	7130	9	HUMPSAA	Sequence
30	24	100.0	40458	9	AC011523	Sequence
31	24	100.0	217346	2	AC027602	Sequence
32	24	100.0	230000	9	AF243527	Sequence
33	20.8	86.7	1514	9	MMPROS	Sequence
34	20	83.3	22	6	AX200977	Sequence
35	20	83.3	22	6	AX267633	Sequence
36	19.8	82.5	2738	5	GU43396	Sequence
37	19.2	80.0	612	6	AX434375	Sequence
38	18.8	78.3	106174	2	AC016126	Sequence
39	18.8	78.3	139389	9	HS6802	Sequence
40	18.8	78.3	158422	9	AC026616	Sequence
41	18.8	78.3	160709	9	AC115837	Sequence
42	18.8	78.3	184516	2	AC009629	Sequence
43	18.4	76.7	1939	9	AK093086	Sequence
44	18.4	76.7	215241	8	AF459639	Sequence
45	18.2	75.8	3806	8	EN1269479	Sequence

ALIGNMENTS

RESULT 1	AX281250	Sequence 7 from Patent WO0176622.	24 bp	DNA	linear	PAT 02-NOV-2001
LOCUS	AX281250	Sequence 7 from Patent WO0176622.				
DEFINITION	AX281250	Sequence 7 from Patent WO0176622.				
ACCESSION	AX281250	Sequence 7 from Patent WO0176622.				
VERSION	AX281250.1	GI:16608506				
KEYWORDS		synthetic construct.				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1	Pedyczak, A., Chong, P. and Sia, C. D.				
AUTHORS		Immunogenic peptides derived from prostate-specific antigen (psa)				
TITLE		and uses thereof				
JOURNAL		Patent: WO 0176622-A 7 18-OCT-2001;				

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Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGTCCCGGTTGCTTCCTC 24
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Db 1 ATGTGGTCCCGGTTGCTTCCTC 24

RESULT 2
AR147236
LOCUS               70 bp DNA linear PAT 08-AUG-2001
DEFINITION          Sequence 2 from patent US 6221579.
ACCESSION            AR147236
VERSION              AR147236.1 GI:15111039
KEYWORDS              Unknown.
SOURCE               Unclassified
ORGANISM              Everhart,D.S. Kaylor,R.M. and McGrath,K.
REFERENCE            1 (bases 1 to 70)
AUTHORS              Patterned binding of functionalized microspheres for optical
TITLE                diffraction-based biosensors
JOURNAL              Patent: US 6221579-A 2 24-APR-2001;
FEATURES             source
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    /organism="unknown"
BASE COUNT           9 a 19 c 23 g 19 t
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Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGTCCCGGTTGCTTCCTC 24
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Db 25 ATGTGGTCCCGGTTGCTTCCTC 48

RESULT 3
HSPSAL
LOCUS               389 bp DNA linear PRI 24-FEB-1999
DEFINITION          Human PSA gene for prostate specific antigen exon 1.
ACCESSION            X13940
VERSION              X13940.1 GI:35722
KEYWORDS              kallikrein; prostate specific antigen; PSA gene.
SOURCE               Homo sapiens.
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS              Digby,M.R.
TITLE                Direct Submission
JOURNAL              Submitted (09-JAN-1989) Digby M.R., The Howard Florey Institute,
REFERENCE            Melbourne University, Parkville, Victoria 3052, Australia
AUTHORS              Digby,M., Zhang,X.Y. and Richards,R.I.
TITLE                Human prostate specific antigen (PSA) gene: structure and linkage
JOURNAL              to the kallikrein-like gene, hGK-1
MEDLINE              Nucleic Acids Res. 17 (5), 2137 (1989)
PUBMED              89183632
COMMENT              2467258
FEATURES             Data kindly reviewed (16-may-1989) by Digby M.R.
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                    /db_xref="taxon:9606"
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                    /clone_lib="cosmid"
                    /note="TATA-box"
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                    204..209
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                    232..>318
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                    232..>318
                    CDS
                    273..>318
                    /note="prostate specific antigen"
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                    /protein_id="CAA32123.1"
                    /db_xref="GI:35723"
                    /db_xref="SWISS-PROT:P07288"
                    /translation="MWVPVFLTSLVTWI"
                    intron
                    318..>389
                    /number=1
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Query Match          100.0%; Score 24; DB 9; Length 389;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGGTCCCGGTTGCTTCCTC 24
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Db 273 ATGTGGTCCCGGTTGCTTCCTC 296

RESULT 4
S75755
LOCUS               569 bp mRNA linear PRI 15-JUN-1995
DEFINITION          PSA-prostate-specific antigen [human, breast cancer specimen, mRNA
ACCESSION            S75755
VERSION              S75755.1 GI:861469
KEYWORDS              Homo sapiens breast cancer specimen.
SOURCE               Homo sapiens
ORGANISM              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
AUTHORS              Monne,M., Croce,C.M., Yu,H. and Diamandis,E.P.
TITLE                Molecular characterization of prostate-specific antigen messenger
JOURNAL              RNA expressed in breast tumors
MEDLINE              Cancer Res. 54 (24), 6344-6347 (1994)
PUBMED              95079406
REMARK              GenBank staff at the National Library of Medicine created this
                    entry [NCBI gibbsq 161505] from the original journal article.
                    Location/Qualifiers
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                    /db_xref="taxon:9606"
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                    /gene="PSA"
                    /note="prostate-specific antigen"
                    1..569
                    /partial
                    /gene="PSA"
                    /note="prostate-specific antigen"
                    /codon_start=3
                    /protein_id="AADI4185.1"
                    /db_xref="GI:4261885"
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                    LGTTCTASGWSIEPEEFLPKLCQCDL"

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BASE COUNT 108 a 182 c 160 g 119 t  
ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 569;  
Best Local Similarity 100.0%; Pred. No. 0.67; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCCTC 24  
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Db 42 ATGTGGTCCCGGTGTCCTC 65

RESULT 5  
HSA310937

LOCUS HSA310937 708 bp mRNA linear PRI 17-JAN-2002  
DEFINITION Homo sapiens mRNA for putative preproPSA-RP2 (KLK3 gene), transcript 1.

ACCESSION AJ310937

VERSION AJ310937.1 GI:14422304  
KEYWORDS alternative splicing; HKLK3 gene; kallikrein 3; preproPSA-RP2.  
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Heuze-Vourc'h, N., Leblond, V., Olayat, S., Gauthier, F. and Courty, Y.  
TITLE Characterization of PSA-RP2, a protein related to prostate-specific antigen and encoded by alternative HKLK3 transcripts  
JOURNAL Eur. J. Biochem. 268 (16), 4408-4413 (2001)

MEDLINE 21393944

PUBMED 11502200

REFERENCE 2 (bases 1 to 708)

AUTHORS Courty, Y.

TITLE Direct Submission

JOURNAL Submitted (11-APR-2001) Courty Y., Faculte de Medecine, EMI-U 0010, Laboratoire d'Enzymologie, 2 bis bd Tonnelle, 37032 Tours cedex, FRANCE

COMMENT related accession number AJ310938.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="NH101007.97"

/cell\_line="LNCap"

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/gene="KLK3"

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/gene="KLK3"

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/gene="KLK3"

/function="unknown"

/note="alternative splicing, transcript 1"

/codon\_start=1

/product="putative preproPSA-RP2"

/protein\_id="CAC41631.1"

/db\_xref="GI:14422305"

/translation="MMVPVFLTSLVTWIGAAPLILSRVGVGWECEKHSOPWQVLVAS

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MSLLKNRFLRPGDSSHDMLLRSEPAELTDAVKVMDLPTQEPALGTTCYASGWGSI

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110..577

/gene="KLK3"

/product="PSA-RP2"

578..708

/gene="KLK3"

708

/gene="KLK3"

/evidence="experimental"

134 a 214 c 219 g 141 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 24; DB 9; Length 708;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCCTC 24

|||||

Db 38 ATGTGGTCCCGGTGTCCTC 61

RESULT 6  
HSA459783

LOCUS HSA459783 870 bp mRNA linear PRI 09-MAY-2002  
DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 2.

ACCESSION AJ459783

VERSION AJ459783.1 GI:20520642

KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Heuze-Vourc'h, N. and Courty, Y.

TITLE Complex alternative splicing of the HKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 870)

AUTHORS Courty, Y.

TITLE Direct Submission

JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire d'Enzymologie, Universite F. Rabelais, 2 bis bd Tonnelle, Tours, 37032 cedex, FRANCE

COMMENT alternative splice variant sequences: AJ459782, AJ459784.

FEATURES

source

Location/Qualifiers

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/db\_xref="taxon:9606"

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/gene="KLK3"

/note="alternative splice variant 2"

/codon\_start=1

/evidence="experimental"

/product="prostate specific antigen"

/protein\_id="CAD30845.1"

/db\_xref="GI:20520643"

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EPEEFLTPKLCQVDLHVISNDVCAQVHPQKTKFNLCAKRWGTXGKSTCGSDGGPLV

CNGVLQGITSWGSEPCALPERPSLYTKVHYRWKIDTIVANP"

22..72

/gene="KLK3"

94..804

/gene="KLK3"

/product="prostate specific antigen"

185 a 257 c 242 g 186 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCCTC 24

|||||

Db 22 ATGTGGTCCCGGTGTCCTC 45

RESULT 7

HSA459782

LOCUS HSN459782 876 bp mRNA linear PRI 09-MAY-2002  
 DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice variant 1.  
 ACCESSION AJ459782  
 VERSION AJ459782.1 GI:20520640  
 KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Heuze-Vourc'h, N. and Courty, Y.  
 TITLE Complex alternative splicing of the hKLK3 gene coding for the tumour marker PSA (prostate-specific-antigen).  
 JOURNAL Unpublished  
 REFERENCE 1 (bases 1 to 876)  
 AUTHORS Courty, Y.  
 JOURNAL Direct Submission  
 TITLE Submitted (03-MAY-2002) Courty, Y., EMI-U 0010, Laboratoire d'Enzymologie, Université F. Rabatelais, 2 bis bdv Tonnelier, Tours, 37032 cedex, FRANCE  
 JOURNAL alternative splice variant sequences: AJ459783, AJ459784.  
 COMMENT Location/Qualifiers  
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 source 1..876  
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 /db\_xref="taxon:9606"  
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 /product="prostate specific antigen"  
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 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Mismatches 24; Conservative 0; Indels 0; Gaps 0;  
 QY 1 ATGTGGTCCCGGTGTCTTCTC 24  
 Db 22 ATGTGGTCCCGGTGTCTTCTC 45  
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 LOCUS HSN17040 990 bp mRNA linear PRI 07-DEC-1994  
 DEFINITION Human prostate specific antigen precursor mRNA, complete cds.  
 ACCESSION U17040  
 VERSION U17040.1 GI:595945  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Monne, M.M., Moreno, J.M., Mele, C.M., Mulholland, G.M. and

Gomella, L.G.  
 TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence in Benign and Malignant Prostate Tissue  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 990)  
 AUTHORS Moreno, J.M.  
 JOURNAL Direct Submission  
 TITLE Submitted (08-NOV-1994) Jose M J.G. Moreno, Urology, Thomas Jefferson University Hospital, 1025 Walnut Street, Philadelphia, PA 19107, USA  
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 sig\_peptide 114..924  
 mat\_peptide 93..113  
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 /protein\_id="AAA56764.1"  
 /note="propeptide"  
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 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Mismatches 24; Conservative 0; Indels 0; Gaps 0;  
 QY 1 ATGTGGTCCCGGTGTCTTCTC 24  
 Db 42 ATGTGGTCCCGGTGTCTTCTC 65  
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 LOCUS I67863 992 bp DNA linear PAT 04-FEB-1998  
 DEFINITION Sequence 13 from patent US 5674682.  
 ACCESSION I67863  
 VERSION I67863.1 GI:2829985  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 992)  
 AUTHORS Fischer, R.; Gomella, L., Mulholland, S. Grant., Moreno, J.G. and Nucleic acid primers for detecting micrometastasis of prostate cancer.  
 TITLE Patent: US 5674682-A 13 07-OCT-1997;  
 JOURNAL Location/Qualifiers  
 FEATURES source 1..992  
 /organism="unknown"  
 BASE COUNT 210 a 291 c 272 g 217 t 2 others  
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 Query Match 100.0%; Score 24; DB 6; Length 992;  
 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Mismatches 24; Conservative 0; Indels 0; Gaps 0;  
 QY 1 ATGTGGTCCCGGTGTCTTCTC 24  
 Db 1 ATGTGGTCCCGGTGTCTTCTC 24



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Db 44 ATGTGGTCCCGGTGTCTTCCTC 67

RESULT 10
HSA459784 1095 bp mRNA linear PRI 09-MAY-2002
LOCUS Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice
DEFINITION variant 3.
ACCESSION AJ459784
VERSION AJ459784.1 GI:20520644
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Heuze-Vourc'h,N. and Courty,Y.
TITLE Complex alternative splicing of the hKLK3 gene coding for the
JOURNAL tumour marker PSA (prostate-specific-antigen)
REFERENCE 2 (bases 1 to 1095)
AUTHORS Courty,Y.
TITLE Direct Submission
JOURNAL Submitted (03-MAY-2002) Courty Y., EMI-U-0010, Laboratoire
d'Enzymologie, Universite F. Rabalais, 2 bis bdv Tonnelles, Tours,
37032 cedex, FRANCE
COMMENT alternative splice variant sequences: AJ459782, AJ459783.
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Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
|||||
Db 38 ATGTGGTCCCGGTGTCTTCCTC 61

RESULT 11
AF335477 1130 bp mRNA linear PRI 13-MAY-2002
LOCUS Homo sapiens prostate-specific antigen variant 1 mRNA, complete
DEFINITION cds, alternatively spliced.
ACCESSION AF335477
VERSION AF335477.1 GI:18478569
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1130)
AUTHORS David,A., Mabyjeesh,N., Azar,I., Biton,S., Engel,S., Bernstein,J.,
Romano,J., Avdor,I., Waks,T., Eshhar,Z., Langer,S.Z.,
Lifschitz-Mercer,B., Matzkin,H., Rotman,G., Toporik,A., Savitsky,K.
and Mintz,L.
Unusual alternative splicing within the human kallikrein genes KLK2
and KLK3 gives rise to novel prostate-specific proteins
J. Biol. Chem. 277 (20), 18084-18090 (2002)
22001285
PUBMED 11834722
REFERENCE 2 (bases 1 to 1130)
AUTHORS David,A., Engel,S., Azar,I., Bernstein,J., Rotman,G., Savitsky,K.
and Mintz,L.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2001) Compugen Ltd., 72 Pinchas Rosen, Tel Aviv
69512, Israel
FEATURES
source
1..1130
/organism="Homo sapiens"
/db_xref="taxon:9606"
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42..356
/notes="PSA; KLK3; alternatively spliced"
/codon_start=1
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Best Local Similarity 100.0%; Pred. No. 0.66;
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QY 1 ATGTGGTCCCGGTGTCTTCCTC 24
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Db 42 ATGTGGTCCCGGTGTCTTCCTC 65

RESULT 12
HUMAPS 1446 bp mRNA linear PRI 04-JAN-1995
LOCUS Homo sapiens prostate-specific antigen mRNA, complete cds.
DEFINITION M26663
ACCESSION M26663
VERSION M26663.1 GI:618463
KEYWORDS prostate-specific antigen.
SOURCE Homo sapiens prostate gland cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Henttu,P. and Viikko,P.
TITLE cDNA coding for the entire human prostate specific antigen shows
JOURNAL high homologies to the human tissue kallikrein genes
MEDLINE Biochem. Biophys. Res. Commun. 160 (2), 903-910 (1989)
89246551
PUBMED 2470373
COMMENT On Jan 5, 1995 this sequence version replaced gi:341511.
Ref [1] reports bases 1..135 only.
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CDS

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Db 25 ATGTGGTCCCGGTGCTCTCCTC 48
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LOCUS
DEFINITION
Sequence 14 from patent US 5674682.
ACCESSION
I67864
VERSION
I67864.1 GI:2829986
KEYWORDS
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 1462)
Croce,C., Gomella,L., Mulholland,S.Grant., Moreno,J.G. and
Fischer,R.
TITLE
Nucleic acid primers for detecting micrometastasis of prostate
cancer
JOURNAL
Patent: US 5674682-A 14 07-OCT-1997;
FEATURES
Location/Qualifiers
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/organism="unknown"
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ORIGIN
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|||||
Db 25 ATGTGGTCCCGGTGCTCTCCTC 48
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LOCUS
DEFINITION
1466 bp RNA linear PAT 31-JAN-2002
Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same.

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VERSION E32812.1 GI:18623942
KEYWORDS JP 2000069969-A/5.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1466)
AUTHORS Nakagawa,H.
TITLE Primer DNA and method for detecting mRNA encoding prostate
gland-specific antigen by using the same
JOURNAL Patent: JP 2000069969-A 5 07-MAR-2000;
COMMENT HITACHI CHEMICAL CO LTD,KK NIHON IDENSHI KENKYUJO
OS Unidentified
PN JP 2000069969-A/5
PP 07-MAR-2000
PR 28-AUG-1998 JP 1998243419
PI HIROKAZU NAKAGAWARA
PC C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
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Db 44 ATGTGGTCCCGGTGCTCTCCTC 67
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DEFINITION Human mRNA for prostate specific antigen.
ACCESSION X05332
VERSION X05332.1 GI:35740
KEYWORDS antigen; kallikrein-like protein; prostate specific antigen; signal
peptide.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1415)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Lundwall,A. and Lilja,H.
JOURNAL Molecular cloning of human prostate specific antigen cDNA
MEDLINE REFS Lett. 214 (2), 317-322 (1987)
PUBMED 87190978
REFERENCE 2 (bases 1 to 1466)
AUTHORS Lundwall,A.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1989)
COMMENT Data kindly reviewed (01-DEC-1987) by Lundwall A.
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44. 829
precursor_RNA
CDS

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95..115
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BASE COUNT 338 a 382 c 422 g 324 t
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Db 44 ATGTGGGTCCCGGTGCTTCCTC 67

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 Job time : 920.641 secs

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XX	40	18.6	77.5	54	21 <th>AAK31468</th> <th>Human cDNA differ</th>	AAK31468	Human cDNA differ
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XX						AAK89250	Human digestive sy

PI Pedyczak A, Chong P, Sia CDY;  
 XX WPI: 2001-663015/76.  
 DR P-PSDB; AAEL3023.  
 XX  
 PM New polypeptide, useful for treating cancers such as prostate cancer,  
 PM comprises prostate-specific antigen derived peptide  
 XX  
 PS Claim 7; Page 28; 41pp; English.  
 CC  
 CC The patent discloses immunogenic peptides of prostate-specific antigen  
 CC (PSA) and nucleic acids encoding them. The peptides of the invention  
 CC are used to prepare a medicament to elicit an immune response in an  
 CC animal. They are used to treat cancer such as prostate cancer and  
 CC tumour metastasis. They are also useful for prophylaxis, for  
 CC preparing monoclonal or polyclonal antibodies, and in conventional  
 CC techniques of immunology, molecular biology, cell biology and  
 CC recombinant DNA technology. The present sequence is a DNA encoding  
 CC PSA derived peptide, CLP313.  
 CC  
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 Db 1 ATGTGGTCCCGGTGTCTTCCTC 24  
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 AC AAT61707;  
 XX  
 DT 24-FEB-1998 (first entry)  
 DE Prostatic specific antigen antisense oligonucleotide.  
 XX  
 KW Human; prostatic specific antigen; probasin; rat; cancer;  
 KW hyperplasia; antisense oligonucleotide; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
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 FT /note= "Phosphorothioated linkages"  
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 MO9711172-AI.  
 PD 27-MAR-1997.  
 XX  
 PD 20-SEP-1996; 96MO-US15123.  
 PF 20-SEP-1996; 96MO-US15123.  
 PR 20-SEP-1995; 95US-0004044.  
 XX  
 PA (WORC-) WORCESTER FOUND BIOMEDICAL RES.  
 XX  
 PI Zamecnik PA;  
 XX  
 DR WPI: 1997-202881/18.  
 XX  
 PT Treatment of benign prostatic hyperplasia or prostatic cancer -  
 PT using an anti-sense oligo:nucleotide targeted against prostate  
 PT specific antigen or the probasin gene  
 XX  
 PS Claim 6; Page 38; 49pp; English.  
 CC A novel method has been developed for treating a patient diagnosed as

CC having benign prostatic hyperplasia or a prostatic cancer. The method  
 CC comprises administering to the patient a therapeutic amount of a  
 CC composition comprising an antisense oligonucleotide which selectively  
 CC hybridises to prostate specific antigen (PSA) gene or mRNA or to a  
 CC probasin gene or mRNA sequence of the patient, where the antisense  
 CC oligonucleotide inhibits expression of the sequence. The present  
 CC sequence represents a specifically claimed antisense oligonucleotide  
 CC against prostatic specific antigen. The antisense oligonucleotide can  
 CC be used to effectively inhibit the growth of (and for the killing of)  
 CC hyperplastic cells or cancerous cells of prostatic origin. Expression  
 CC of the PSA and probasin genes is specific to prostate cells so that the  
 CC antisense oligonucleotide can be administered systemically, making it  
 CC particularly useful in late stage prostatic cancer which has  
 CC metastasised, and in which the cells have become resistant to oestrogen  
 CC or anti-androgen therapy. The method can also be used in benign prostate  
 CC hyperplasia, or early stage prostatic cancer, as an alternative for the  
 CC more radical procedures currently used, such as transurethral resection,  
 CC radical prostatectomy, or physical or chemical castration.  
 CC  
 XX  
 S0 Sequence 27 BP; 9 A; 7 C; 9 G; 2 T; 0 other;  
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 Db 27 ATGTGGTCCCGGTGTCTTCCTC 4  
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 ID AAT35293 standard; DNA; 45 BP.  
 AC AAT35293;  
 XX  
 DT 11-MAR-1997 (first entry)  
 DE Forward primer F1 for prostate specific antigen.  
 XX  
 KW Polymerase chain reaction; primer; amplify; prostate specific antigen;  
 KW baculovirus transfer vector; PCR; PSA; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT modified\_base 1..27  
 FT /\*tag= a  
 FT /note= "Phosphorothioated linkages"  
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 MO9711172-AI.  
 PD 27-MAR-1997.  
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 PD 20-SEP-1996; 96EP-0101304.  
 PF 20-SEP-1996; 96EP-0101304.  
 PR 28-APR-1995; 95US-0430498.  
 PR 03-FEB-1995; 95US-0383111.  
 XX  
 PA (FARB ) BAYER CORP.  
 XX  
 PI Barnett TR, Ng PC, Yeung KK;  
 XX  
 DR WPI: 1996-356106/36.  
 XX  
 PT Recombinant prostate-specific antigen (PSA) and immunological  
 PT fragments - for use as an immunoassay calibrator in commercial PSA  
 PT tests.  
 XX  
 PS Claim 3; Page 5; 19pp; English.  
 CC  
 CC AAT35293-r35295 represent amplification primers for the prostate  
 CC specific antigen (PSA). These primers were used to insert the cDNA for  
 CC PSA into a BamHI-NotI-cleaved pVL1393 baculovirus transfer vector. The  
 CC vector that was produced is ATCC VR-2495. The rPSA can produced by the  
 CC use the rPSA are for the quantitative determination of PSA in a  
 CC biological sample. In the assay, the test sample is combined with a



Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24  
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Db 25 ATGTGGTCCCGGTTGCTTCCTC 48

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AC ABL60747;  
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DT 10-SEP-2002 (first entry)  
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DE Prostate specific antigen (PSA) fragment encoding DNA.  
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KM Prostate specific antigen; PSA; prostate; cancer; prostatic disease;  
XX gene; ds.  
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OS Unidentified.  
XX  
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FT FT /\*product= "PSA"  
FT FT /\*note= "partial fragment"  
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FT FT /\*note= "preproPSA"  
FT FT 52..72  
FT FT /\*tag= c  
FT FT /\*note= "PropSA"  
FT FT 73..90  
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FT FT /\*note= "partial mature PSA"  
XX  
PN US2002045198-A1.  
XX  
PD 18-APR-2002.  
XX  
PF 23-FEB-2001; 2001US-0792534.  
XX  
PR 30-APR-1999; 99US-0302965.  
XX  
PA (MIKO/) MIKOLAJCZYK S D.  
PA (RITT/) RITTENHOUSE H G.  
PA (WANG/) WANG T J.  
PA (WOLF/) WOLFERT R L.  
XX  
PI Mkolajczyk SD, Rittenhouse HG, Wang TJ, Wolfert RL;  
XX WPI: 2002-425439/45.  
XX  
DR P-PSDB; ABB08071.  
XX  
PT Determining prostate specific antibody (PPSA), comprises determining  
PT the amount of complex formed on treating a sample with a PSA specific  
PT antibody, useful for detecting prostate cancer and distinguishing it  
PT from benign prostatic disease  
XX  
PS Disclosure; Fig 1; 30pp; English.  
XX  
CC The invention provides a method of determining prostate specific antigen  
CC (PPSA) in a sample which involves determining the amount of complex  
CC formed on treating a sample with a PSA specific antibody. The method is  
CC useful for detecting prostate cancer and distinguishing it from benign  
CC prostatic disease. The present sequence represents a DNA encoding a  
CC partial fragment of the PSA.  
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SQ Sequence 90 BP; 8 A; 26 C; 31 G; 25 T; 0 other;  
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGGTCCCGGTTGCTTCCTC 24

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AC AAT92974;  
XX  
DT 24-APR-1998 (first entry)  
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DE cDNA for prostate specific antigen (PSA).  
XX  
KM Diagnosis; prostate cancer; prostate specific antigen; PSA;  
KM metastatic prostate cancer; prostate cell; secondary tumour;  
XX bone metastatic anchoring; ss.  
XX  
OS Homo sapiens.  
XX  
FH WO9739139-A1.  
XX  
PD 23-OCT-1997.  
XX  
PF 16-APR-1997; 97WO-US06497.  
XX  
PR 16-APR-1996; 96US-0015765.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Robbins DJ;  
XX  
DR WPI: 1997-526473/48.  
XX  
PT Monitoring or diagnosis of prostate cancer - by detecting  
PT prostate-specific antigen mRNA using specific primers  
XX  
PS Disclosure; Page 13; 25pp; English.  
XX  
CC cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).  
CC The detection of PSA mRNA in peripheral blood is associated with  
CC metastatic prostate cancer. Detection of PSA mRNA in the bloodstream  
CC indicates that prostate cells are circulating in the blood and confirms  
CC diagnosis of cancer. Circulating prostate cells also indicate a risk of a  
CC secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA  
CC after prostatectomy or radiotherapy indicates a risk that the prostate  
CC cancer has spread and that the surgery and radiotherapy was not  
CC effective. PCR primers AAT92971-73 were used for the monitoring and  
CC diagnosis of patients with prostate cancer. The method comprises the  
CC detection of PSA mRNA by reverse transcriptase polymerase chain reaction  
CC (RT-PCR).  
XX  
SQ Sequence 92 BP; 14 A; 28 C; 28 G; 22 T; 0 other;  
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Best Local Similarity 100.0%; Pred. No. 0.17;  
XX  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
Db 38 ATGTGGTCCCGGTTGCTTCCTC 61  
XX  
RESULT 8  
AAT35294  
ID AAT35294 standard; DNA; 93 BP.  
XX  
AC AAT35294;  
XX



DT 11-MAR-1997 (first entry)  
XX Forward primer F2 for prostate specific antigen.  
DE Polymerase chain reaction; primer; amplify; prostate specific antigen;  
XX baculovirus transfer vector; PCR; PSA; ss.  
KM Synthetic.  
XX EP725139-A2.  
XX 07-AUG-1996.  
XX 31-JAN-1996; 96EP-0101304.  
PF 28-APR-1995; 950S-0430498.  
PR 03-FEB-1995; 950S-0383111.  
XX (FARB ) BAYER CORP.  
XX Barnett TR, Ng PC, Yeung KK;  
PI WPI; 1996-356106/36.  
DR Recombinant prostate-specific antigen (PSA) and immunological  
XX fragments - for use as an immunoassay calibrator in commercial PSA  
PT tests.  
PT Claim 3; Page 5; 19pp; English.  
PS AAT3293-T35295 represent amplification primers for the prostate  
XX specific antigen (PSA). These primers were used to insert the cDNA for  
CC PSA into a BamHI-NOTI-cleaved pVL393 baculovirus transfer vector. The  
CC vector that was produced is ATCC VR-2496. The PSA can be produced by the  
CC use of the rPSA are for the quantitative determination of PSA in a  
CC biological sample. In the assay, the test sample is combined with a  
CC labelled conjugate and the response of the conjugate is compared with a  
CC standard curve established by performing the assay on one or more  
CC calibrators using rPSA (or an immunologically reactive fragment).  
XX Sequence 93 BP; 12 A; 23 C; 31 G; 27 T; 0 other;  
SQ  
Query Match 100.0%; Score 24; DB 17; Length 93;  
Best Local Similarity 100.0%; Pred. No. 0.17; Mismatches 0; Gaps 0;  
Matches 24; Conservative 0; Indels 0; Gaps 0;  
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Db 16 ATGTGGGTCCCGGTGTCTTCCTC 39  
RESULT 9  
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ID ABV07911 standard; cDNA; 171 BP.  
XX  
AC ABV07911;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 7902.  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KM pharmacogenomic marker; gene; ss.  
XX Homo sapiens.  
OS  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX

PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
XX Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
DR  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer  
XX  
PS Claim 1; Page 1267; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
XX (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
SQ  
Sequence 171 BP; 20 A; 55 C; 51 G; 43 T; 2 other;  
SQ  
Query Match 100.0%; Score 24; DB 23; Length 171;  
Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Gaps 0;  
Matches 24; Conservative 0; Indels 0; Gaps 0;  
QY 1 ATGTGGGTCCCGGTGTCTTCCTC 24  
Db 79 ATGTGGGTCCCGGTGTCTTCCTC 102  
RESULT 10  
ABV07396  
ID ABV07396 standard; cDNA; 308 BP.  
XX  
AC ABV07396;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 7387.  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KM pharmacogenomic marker; gene; ss.  
XX Homo sapiens.  
OS  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
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PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX

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XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
PI WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 1194; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 308 BP; 65 A; 100 C; 79 G; 63 T; 1 other;
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Query Match 100.0%; Score 24; DB 23; Length 308;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTGTCTTCTC 24
DB 198 ATGTGGTCCCGGTGTCTTCTC 221
XX
XX RESULT 11
XX ABV37330
XX ID ABV37330 standard; cDNA; 428 BP.
XX AC
XX AC ABV37330;
XX AC
XX DT 16-SEP-2002 (first entry)
XX DT
XX DE Human prostate expression marker cDNA 37321;
XX DE
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX OS
XX PM WO200160860-A2.
XX PM
XX PD 23-AUG-2001.
XX PD
XX PF 20-FEB-2001; 2001WO-US05171.
XX PF
XX PR 17-FEB-2000; 2000US-183319P.
XX PR
XX PR 16-MAR-2000; 2000US-189862P.
XX PR
XX PR 25-MAY-2000; 2000US-207454P.
XX PR
XX PR 09-JUN-2000; 2000US-211314P.
XX PR
XX PR 18-JUL-2000; 2000US-219007P.
XX PR
XX PR 13-DEC-2000; 2000US-255281P.
XX PR
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
PI WPI: 2001-662795/76.
XX
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```
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX Claim 1; Page 7668; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 428 BP; 82 A; 132 C; 123 G; 91 T; 0 other;
SQ
Query Match 100.0%; Score 24; DB 23; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTGTCTTCTC 24
DB 271 ATGTGGTCCCGGTGTCTTCTC 294
XX
XX RESULT 12
XX AAA61482
XX ID AAA61482 standard; DNA; 517 BP.
XX AC
XX AC AAA61482;
XX AC
XX DT 23-OCT-2000 (first entry)
XX DT
XX DE Prostate specific antigen gene fragment.
XX DE
XX KW Isothermal DNA amplification; nucleic acid synthesis; detection;
XX KW PSA gene template; prostate specific antigen; human; ds.
XX OS Homo sapiens.
XX OS
XX PN WO200028082-A1.
XX PN
XX PD 18-MAY-2000.
XX PD
XX PF 08-NOV-1999; 99WO-JP06213.
XX PF
XX PR 09-NOV-1998; 98JP-0317476.
XX PR
XX (EIKE ) EIKEN KAGAKU KK.
XX PA
XX PI Notomi T, Hase T;
XX PI
XX DR WPI: 2000-376587/32.
XX DR
XX Nucleic acid synthesis using primer containing a sequence identical to
PT one on the template for isothermal amplification using simple reagents
PT
XX Example 8; Fig 17; 95pp; Japanese.
XX
XX The invention relates to a novel method of isothermal DNA amplification.
CC A region is produced at the 3' end of a target sequence which contains
CC sub-sequences designated FI, F2C and FIC, where FIC is the complement of
CC FI. A loop is formed by annealing of FI to its complementary sequence
```



Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rng

Page 8

Db 62 ATGTGGTCCGGTGTCTCTCCTC 85

RESULT 15

AAZ47134  
ID AAZ47134 standard; DNA; 990 BP.

AC AAZ47134;

DT 28-MAR-2000 (first entry)

DE Human prostate-specific antigen gene.

KW Immunization; prostate cancer; prostate-specific antigen; PSA;

OS cytosolic; immune response; ds.

PN Homo sapiens.

PD WO9961068-A1.

PE 02-DEC-1999.

PF 28-MAY-1999; 99WO-US12072.

PR 29-MAY-1998; 98US-0087305.

FA (TYPE-) UNIV PENNSYLVANIA.

PI Weiner DB, Kim JJ;

DR WPI; 2000-072551/06.

XX P-PSDB; AAY56048.

PT Immunization against prostatic cancer using nucleic acid encoding

XX prostate-specific antigen, for treatment or prophylaxis

PS Disclosure; Page 42; 47pp; English.

CC The invention relates to a method of immunization against prostatic

CC cancer (PC) by administering a nucleic acid (this sequence) that encodes

CC prostate-specific antigen (PSA), or its immunologically active fragment

CC operably linked to regulatory sequences. The nucleic acid is taken up by

CC cells and then expressed to generate an immune response against PSA.

CC The method is used to protect against, or treat, PC, or more generally

CC to induce a cellular immune response to PSA.

XX

SO Sequence 990 BP; 209 A; 291 C; 273 G; 217 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 990;

Best Local Similarity 100.0%; Pred No. 0.21; 0;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCGGTGTCTCTCCTC 24

DB 42 ATGTGGTCCGGTGTCTCTCCTC 65

Search completed: November 19, 2002, 03:06:36

Job time: 171.462 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 ; Search time 1371.08 Seconds  
(without alignments)  
283.494 Million cell updates/sec

Title: US-09-829-004A-7

Perfect score: 24

Sequence: 1 atggtgcgcgcgtgtctctctc

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308132

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
EST :  
1: em\_estba:\*  
2: em\_estbm:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_estl3:\*  
13: gb\_estl4:\*  
14: gb\_estl5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_luv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	316	9	AA593245
2	24	100.0	336	9	AA506459
3	24	100.0	371	9	AA503943
4	24	100.0	391	9	AA506939
5	24	100.0	408	12	BF678836
6	24	100.0	457	9	AA528287

7	24	100.0	465	13	B1046475	
c <td>8</td> <td>24</td> <td>100.0</td> <td>495</td> <td>12</td> <td>BE840533</td>	8	24	100.0	495	12	BE840533
c <td>9</td> <td>24</td> <td>100.0</td> <td>505</td> <td>12</td> <td>BE840441</td>	9	24	100.0	505	12	BE840441
10	24	100.0	523	9	AA639901	
11	24	100.0	532	12	BE840701	
c <td>12</td> <td>24</td> <td>100.0</td> <td>572</td> <td>12</td> <td>BE840537</td>	12	24	100.0	572	12	BE840537
13	24	100.0	591	12	BF679591	
14	24	100.0	638	12	BF679511	
15	24	100.0	648	12	BF67605	
16	24	100.0	672	9	A1524893	
17	24	100.0	724	12	BE964653	
18	24	100.0	732	9	A1547309	
19	24	100.0	737	9	A1547285	
20	24	100.0	748	12	BF679168	
21	24	100.0	748	12	BE973983	
22	24	100.0	756	12	BE676011	
23	24	100.0	763	12	BF965254	
24	24	100.0	770	12	BF675749	
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29	24	100.0	797	12	BF675142	
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31	24	100.0	825	12	BF677556	
32	24	100.0	828	12	BF678076	
33	24	100.0	832	9	A1557311	
34	24	100.0	838	12	BF680970	
35	24	100.0	841	12	BF673766	
36	24	100.0	843	12	BF675323	
37	24	100.0	849	12	BF673243	
38	24	100.0	859	12	BF675660	
39	24	100.0	860	12	BE675331	
40	24	100.0	866	12	BE965220	
41	24	100.0	868	12	BF673807	
42	24	100.0	871	12	BF673369	
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45	24	100.0	890	14	BQ949420	

#### ALIGNMENTS

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mRNA sequence.  
ACCESSION AA593245 316 bp mRNA  
VERSION AA593245.1 GI:2409007  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 316)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapdb-remail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,  
Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www.bio.lnl.gov/bdrp/image/image.html  
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Location/Qualifiers

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ACCESSION AA506459.1 GI:2242699  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 336)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,  
M.D. Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA library preparation: David B. Krizman, Ph.D.  
CDNA library arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bdrp/image/image.html  
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## FEATURES

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mRNA sequence.

ACCESSION AA503943  
VERSION  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 371)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,  
M.D. Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA library preparation: David B. Krizman, Ph.D.  
CDNA library arrayed by: Greg Lennon, Ph.D.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
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www-bio.llnl.gov/bdrp/image/image.html  
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Location/Qualifiers

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112 c 111 g 85 t

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 VERSION AA506939.1  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 391)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuagui,  
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
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 NIH-MGC <http://mhc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: CLONETECH Laboratories, Inc.  
 CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.lnl.gov>  
 Plate: L1CM1143 row: e column: 11  
 High quality sequence stop: 407  
 BASE COUNT 74 a 127 c 115 g 92 t  
 ORIGIN  
 1..408  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4294258"  
 /clone\_lib="NIH\_MGC\_83"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site\_1: SfiI (ggcgcttcggcc); Site\_2: SfiI (ggccatagcc  
 ); 5' and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor  
 sequence: 5'-ATTCTAGAGCGCGAGCGCGGCACATG-dT(30)BN-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA)."  
 Query Match 100.0%; Score 24; DB 12; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 24; Conservative 0; Mismatches 0;  
 QY 1 ATGTGGTCCCGGTGTCTCTC 24  
 ||||||||||||||||||||  
 Db 37 ATGTGGTCCCGGTGTCTCTC 60  
 RESULT 6  
 LOCUS AA528287 457 bp mRNA linear EST 20-AUG-1997  
 DEFINITION nh2608.s1 NCI CGAP Pr3 Homo sapiens cDNA clone IMAGE:953487  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,  
 mRNA sequence.  
 ACCESSION AA528287  
 VERSION AA528287.1 GI:2270356  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 457)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,  
 Michael Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)  
 Seq primer: -40m13 fwd. ET from AmerSham  
 High quality sequence stop: 187  
 BASE COUNT 115 a 147 c 187 g 118 t  
 ORIGIN  
 1..457  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:953487"  
 /clone\_lib="NCI\_CGAP\_Pr3"  
 /sex="male"

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/dev.stage="45 years old"
/lab.host="PH10B"
/Note="Vector: PAMP10: Site.1: Not1: Site.2: EcoRI: 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDC-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."

BASE COUNT      79 a      160 c      112 g      106 t
ORIGIN
Query Match      100.0%; Score 24; DB 9; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGGTCGCCGGTGTCTTCCTC 24
|||||
Db 26 ATGTGGGTCGCCGGTGTCTTCCTC 49

RESULT 7
LOCUS      B1046475      465 bp      mRNA      linear      EST 14-JUN-2001
DEFINITION      MR3-FN0209-070201-010-b11 FN0209 Homo sapiens cDNA, mRNA sequence.
ACCESSION      B1046475
VERSION      B1046475.1 GI:14453097
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 465)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3&l2=MR3-FN0209-
070201-010-b11&l3=2001-02-07&l4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 465.
Location/Qualifiers
1. 465
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0209"
/dev_stage="Adult"
/Note="Organ: prostate.normal; Vector: puc18; Site.1: SmaI
; Site.2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196.716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse

BASE COUNT      125 a      161 c      131 g      77 t
ORIGIN
Query Match      100.0%; Score 24; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGGTCGCCGGTGTCTTCCTC 24
|||||
Db 463 ATGTGGGTCGCCGGTGTCTTCCTC 440

transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT      83 a      134 c      144 g      103 t
ORIGIN
Query Match      100.0%; Score 24; DB 13; Length 465;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGGTCGCCGGTGTCTTCCTC 24
|||||
Db 167 ATGTGGGTCGCCGGTGTCTTCCTC 190

RESULT 8
LOCUS      BE840533/c      495 bp      mRNA      linear      EST 22-SEP-2000
DEFINITION      R01-FN0188-260700-022-F06 FN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BE840533
VERSION      BE840533.1 GI:10272911
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 495)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=R01-FN0188-260
700-022-F06&l3=2000-07-26&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 495.
Location/Qualifiers
1. 495
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="FN0188"
/dev_stage="Adult"
/Note="Organ: prostate.normal; Vector: puc18; Site.1: SmaI
; Site.2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196.716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

```



RESULT 9  
BE840441/c 505 bp mRNA linear EST 22-SEP-2000  
LOCUS R01-FN0188-210700-021-a02 FN0188 Homo sapiens CDNA, mRNA sequence.  
DEFINITION BE840441  
ACCESSION BE840441.1 GI:10272819  
VERSION EST.  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 505)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
2020263  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=6&2=R01-FN0188-210  
700-021-a02&t3=2000-07-21&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 505.  
Location/Qualifiers  
1..505  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="FN0188"  
/dev\_stage="Adult"  
/note="Organ: prostate.normal; Vector: puc18; Site\_1: SmaI  
; Site\_2: SmaI; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196/716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."  
BASE COUNT 127 a 164 c 136 g 78 t  
ORIGIN  
Query Match 100.0%; Score 24; DB 12; Length 505;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTGGTCCCGGTGTCTCTC 24  
|||||  
Db 460 ATGTGGTCCCGGTGTCTCTC 437  
RESULT 10  
AA639901 523 bp mRNA linear EST 23-OCT-1997  
LOCUS np08f03.s1 NCI-CCAP\_Pr3 Homo sapiens CDNA clone IMAGE:1115741  
DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,  
RNA sequence.  
ACCESSION AA639901 GI:2563680  
VERSION AA639901.1  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 523)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagut, M.D.  
Michael Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/birp/image/image.html  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 367.  
Location/Qualifiers  
1..523  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:1115741"  
/clone\_lib="NCI-CCAP\_Pr3"  
/sex="Male"  
/dev\_stage="45 years old"  
/lab\_host="DH10B"  
/note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st  
strand cDNA was primed with oligo(dT)17 on 50 ng of  
DNase-treated, total cellular RNA obtained from 5,000-10,  
000 microdissected cells histologically determined to be  
fully malignant prostate cancer cells. Double-stranded  
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR  
applied to the cDNA with an adaptor-specific primer, and  
the resulting PCR product subcloned into PAMP10 by the  
UDG-cloning method (Life Technologies). Average insert  
size is 600 bp. NOTE: Not directionally cloned. This  
library was constructed by David Kitzman."  
BASE COUNT 100 a 160 c 152 g 111 t  
ORIGIN  
Query Match 100.0%; Score 24; DB 9; Length 523;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGTGGTCCCGGTGTCTCTC 24  
|||||  
Db 32 ATGTGGTCCCGGTGTCTCTC 55  
RESULT 11  
BE840701 552 bp mRNA linear EST 22-SEP-2000  
LOCUS R01-FN0188-140800-011-g05 FN0188 Homo sapiens CDNA, mRNA sequence.  
DEFINITION BE840701  
ACCESSION BE840701.1 GI:10273079  
VERSION EST.  
KEYWORDS human.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL

**MEDLINE** 20202663  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RCL-FN0188-140>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 2  
 High quality sequence stop: 552.  
 Location/Qualifiers

**FEATURES**  
 source  
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 /db\_xref="taxon:9606"  
 /clone\_lib="FN0188"  
 /dev\_stage="Adult"  
 /note="Organ: prostate,normal; Vector: puc18; Site\_1: Sma1  
 ; Site\_2: Sma1; A mini-library was made by cloning  
 products derived from ORESTES PCR (U.S. Letters Patent  
 application No. 196,716 - Ludwig Institute for Cancer  
 Research) profiles into the puc 18 vector. Reverse  
 transcription of tissue mRNA and cDNA amplification were  
 performed under low stringency conditions."

**BASE COUNT** 79 a 150 c 171 g 152 t

**ORIGIN**

Query Match 100.0%; Score 24; DB 12; Length 552;  
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 12**  
**LOCUS** BE840537 572 bp mRNA linear EST 22-SEP-2000  
**DEFINITION** RCL-FN0188-260700-022-h06 FN0188 Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BE840537  
**VERSION** BE840537.1 GI:10272915  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;  
 1 (bases 1 to 572)  
 Dias Neto E., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,  
 Nagai M.A., de Silva M. Jr., Zago M.A., Bordin S., Costa F.F.,  
 Goldman G.H., Carvalhal A.F., Matsukuma A., Bala G.S., Simpson D.H.,  
 Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare  
 M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and  
 Simpson A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

**JOURNAL** MEDLINE  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RCL-FN0188-260700-022-h06&tl3=2000-07-26&tl4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 10  
 High quality sequence stop: 572.  
 Location/Qualifiers

**FEATURES**  
 source  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FN0188"  
 /dev\_stage="Adult"  
 /note="Organ: prostate,normal; Vector: puc18; Site\_1: Sma1  
 ; Site\_2: Sma1; A mini-library was made by cloning  
 products derived from ORESTES PCR (U.S. Letters Patent  
 application No. 196,716 - Ludwig Institute for Cancer  
 Research) profiles into the puc 18 vector. Reverse  
 transcription of tissue mRNA and cDNA amplification were  
 performed under low stringency conditions."

**BASE COUNT** 156 a 175 c 156 g 85 t

**ORIGIN**

Query Match 100.0%; Score 24; DB 12; Length 572;  
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 13**  
**LOCUS** BF679591 591 bp mRNA linear EST 21-DEC-2000  
**DEFINITION** 60215403F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4294929 5',  
 mRNA sequence.  
**ACCESSION** BF679591  
**VERSION** BF679591.1 GI:11953486  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo;  
 1 (bases 1 to 591)  
 NIH-MGC <http://mgs.nci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: CLONETECH Laboratories, Inc.  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Pile: LNCMI45 row: a column: 10  
 High quality sequence stop: 587.  
 Location/Qualifiers

**FEATURES**  
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 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:4294929"  
 /clone\_lib="NIH\_MGC\_83"  
 /lab\_host="DH10B (71 phage-resistant)"  
 /note="Organ: prostate; Vector: pNR-LIB (Clontech);  
 Site\_1: SfiI (ggcgccctgcgc); Site\_2: SfiI (ggcgctatggcc  
 ); 5' and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-ATCTAGAGCGCGCGCGCGCGCAGC-AT(30)BN-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech

BASE COUNT 116 a 181 c 166 g 128 t  
ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 591;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTCCTC 24  
|||||  
DB 37 ATGTGGGTCCCGGTGTCTCTCCTC 60

RESULT 14  
BF679511 638 bp mRNA linear EST 21-DEC-2000  
LOCUS 602153922P1 NIH\_MGC\_83 Homo sapiens cDNA IMAGE:4295164 5',  
DEFINITION mRNA sequence.  
ACCESSION BF679511  
VERSION BF679511  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM1145 row: k column: 05  
High quality sequence stop: 633.  
Location/Qualifiers  
1. 638  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4295164"  
/clone\_lib="NIH\_MGC\_83"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggccgctgccc); Site 2: SfiI (ggccatgatgccc  
); 5' and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3',  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 86 a 190 c 182 g 180 t  
ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 638;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTCCTC 24  
|||||  
DB 43 ATGTGGGTCCCGGTGTCTCTCCTC 66

RESULT 15  
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LOCUS 602085679P1 NIH\_MGC\_83 Homo sapiens cDNA IMAGE:4249939 5',  
DEFINITION

mRNA sequence.  
BF677605  
BF677605.1 GI:11951500  
EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM1070 row: n column: 20  
High quality sequence stop: 611.  
Location/Qualifiers  
1. 648  
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/db\_xref="taxon:9606"  
/clone="IMAGE:4249939"  
/clone\_lib="NIH\_MGC\_83"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggccgctgccc); Site 2: SfiI (ggccatgatgccc  
); 5' and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGACATG-dT(30)BN-3',  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

BASE COUNT 124 a 198 c 185 g 141 t  
ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 648;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTCCTC 24  
|||||  
DB 43 ATGTGGGTCCCGGTGTCTCTCCTC 66

Search completed: November 19, 2002, 05:17:29  
Job time : 1377.08 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 47.0769 seconds  
(without alignments)  
156.345 Million cell updates/sec

Title: US-09-829-004A-7

Perfect score: 24  
Sequence: 1 atgtgggtccggtgtgtctctc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
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6: /cgn2\_6/prodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	24	100.0	111	1	US-08-454-720A-42
3	24	100.0	992	1	US-08-358-782D-13
4	24	100.0	992	2	US-08-764-527A-13
5	24	100.0	1462	1	US-08-358-782D-14
6	24	100.0	1462	2	US-08-764-527A-14
7	24	100.0	7130	4	US-09-056-105-31
8	20	83.3	22	4	US-09-605-785-607-
9	18	75.0	28	1	US-08-394-033-1
10	18	75.0	2153	2	US-08-577-492-31
11	18	75.0	2153	4	US-09-079-630-31
12	17.6	73.3	1348	4	US-09-042-071-19
13	16.4	68.3	1864	4	US-08-454-720A-38
14	16	66.7	72	4	US-08-983-075D-10
15	16	66.7	558	4	US-09-385-982-435
16	16	66.7	832	4	US-09-100-264-8
17	16	66.7	832	3	US-08-768-859A-5
18	16	66.7	832	3	US-08-768-859A-20
19	16	66.7	832	3	US-08-767-820A-5
20	16	66.7	832	3	US-08-767-820A-20
21	16	66.7	832	3	US-08-622-046B-4
22	16	66.7	832	3	US-08-622-046B-15
23	16	66.7	832	5	PCT-US95-06157-5
24	16	66.7	833	2	US-08-790-137-2
25	16	66.7	833	1	US-08-744-026-2
26	16	66.7	871	2	US-09-102-732-2
27	16	66.7	871	4	US-09-261-767-2

28	16	66.7	871	4	US-08-969-987-7	Sequence 7, Appl
29	16	66.7	1279	3	US-08-985-950-5	Sequence 5, Appl
30	16	66.7	1341	4	US-08-983-075D-6	Sequence 6, Appl
31	16	66.7	1358	4	US-08-983-075D-8	Sequence 8, Appl
32	16	66.7	1728	3	US-08-985-950-7	Sequence 7, Appl
33	15.8	65.8	424	1	US-08-158-189-4	Sequence 4, Appl
34	15.8	65.8	2880	1	US-08-158-189-1	Sequence 1, Appl
35	15.6	65.0	340	4	US-08-836-075A-99	Sequence 9, Appl
36	15.6	65.0	1508	4	US-09-404-390-14	Sequence 15, Appl
37	15.6	65.0	2333	4	US-09-404-390-15	Sequence 2, Appl
38	15.6	65.0	8051	2	US-08-576-626A-2	Sequence 10, Appl
39	15.2	63.3	1512	2	US-07-938-154-10	Sequence 10, Appl
40	15.2	63.3	1512	5	PCT-US91-02311-10	Sequence 10, Appl
41	15.2	63.3	2241	2	US-08-838-219B-20	Sequence 20, Appl
42	15.2	63.3	2241	3	US-09-233-336A-20	Sequence 20, Appl
43	15.2	63.3	2241	3	US-09-233-752A-20	Sequence 20, Appl
44	15.2	63.3	2241	4	US-09-402-036-20	Sequence 20, Appl
45	15.2	63.3	2241	4	US-09-904-226-20	Sequence 20, Appl

#### ALIGNMENTS

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RESULT 1
US-09-210-016-2
: Sequence 2, Application US/09210016
: Patent No. 6221579
: GENERAL INFORMATION:
: APPLICANT: Everhart, Dennis S.
: APPLICANT: Kaylor, Rosann M.
: APPLICANT: McGeath, Kevin
: TITLE OF INVENTION: Patterned Binding of Functionalized Microspheres for
: TITLE OF INVENTION: Optical Diffraction-based Biosensors
: FILE REFERENCE: 11301-0880
: CURRENT APPLICATION NUMBER: US/09/210,016
: CURRENT FILING DATE: 1998-12-11
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2
: LENGTH: 70
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Oligonucleotide
US-09-210-016-2
Query Match 100.0%; Score 24; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No.: 0.022;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTCCCGGTGCTCTCTC 24
Db 25 ATGTGGTCCCGGTGCTCTCTC 48
RESULT 2
US-08-454-720A-42
: Sequence 42, Application US/08454720A
: Patent No. 5766888
: GENERAL INFORMATION:
: APPLICANT: Sobol, Robert E.
: APPLICANT: Green, Mark R.
: APPLICANT: Kawasaki, Ernest S.
: TITLE OF INVENTION: Detection of Carcinoma Metastases by
: TITLE OF INVENTION: Nucleic Acid Amplification
: NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffman-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: U.S.A.
```

Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rni

Page 2

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ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.01, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,720A
FILING DATE: May 31, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/357,565
FILING DATE: December 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas
REGISTRATION NUMBER: 35321
REFERENCE/DOCKET NUMBER: 9178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-720A-42

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Best Local Similarity 100.0%; Pctd. No. 0.023;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ATGTGGTCCCGGTTGTCTTCTC 24
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Db 1 ATGTGGTCCCGGTTGTCTTCTC 24

RESULT 3
US-08-358-782D-13
Sequence 13, Application US/08358782D
Patent No. 5674682
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Gomella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782D
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TJU-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:

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SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-358-782D-13

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Best Local Similarity 100.0%; Score 24; DB 1; Length 992;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCGGTGTCTCTCTC 24
Db 44 ATGTGGTCCGGTGTCTCTCTC 67

RESULT 4
US-08-764-527A-13
Sequence 13, Application US/08764527A
Patent No. 5939258
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Comella, Leonard
APPLICANT: Mulholland, S. Grant
APPLICANT: Moreno, Jose
APPLICANT: Fischer, Rainer
TITLE OF INVENTION: Methods of Detecting Micrometastasis of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place 46th. Floor
CITY: Philadelphia
STATE: PA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,527A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,782
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: TUD-1327
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-764-527A-13

Query Match
Best Local Similarity 100.0%; Score 24; DB 2; Length 992;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGTGGTCCGGTGTCTCTCTC 24
Db 44 ATGTGGTCCGGTGTCTCTCTC 67

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Db 44 ATGTGGGTCCCGGTGTCTCTC 67

RESULT 5

US-08-358-782D-14

Sequence 14, Application US/08358782D

Patent No. 5674682

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

APPLICANT: Gomeila, Leonard

APPLICANT: Mulholland, S. Grant

APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer

TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

CITY: Philadelphia

STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,782D

FILING DATE: 15-DEC-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: TJU-1327

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1462 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-358-782D-14

Query Match 100.0%; Score 24; DB 1; Length 1462;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 ATGTGGGTCCCGGTGTCTCTC 48

RESULT 6

US-08-764-527A-14

Sequence 14, Application US/08764527A

Patent No. 5939258

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

APPLICANT: Gomeila, Leonard

APPLICANT: Mulholland, S. Grant

APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer

TITLE OF INVENTION: Methods of Detecting Micrometastasis of

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

STREET: One Liberty Place 46th. Floor

CITY: Philadelphia

STATE: PA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,527A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/358,782

FILING DATE: 15-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

REFERENCE/DOCKET NUMBER: TJU-1327

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 1462 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-764-527A-14

Query Match 100.0%; Score 24; DB 2; Length 1462;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTC 24

Db 25 ATGTGGGTCCCGGTGTCTCTC 48

RESULT 7

US-09-056-105-31

Sequence 31, Application US/09056105

Patent No. 6287569

GENERAL INFORMATION:

APPLICANT: KIPPS, THOMAS J.

APPLICANT: MU, YUNQI

TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR

FILE REFERENCE: 233/221

CURRENT APPLICATION NUMBER: US/09/056,105

CURRENT FILING DATE: 1998-04-06

EARLIER APPLICATION NUMBER: 60/043,467

EARLIER FILING DATE: 1997-04-10

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 7130

TYPE: DNA

ORGANISM: Homo sapiens

US-09-056-105-31

Query Match 100.0%; Score 24; DB 4; Length 7130;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTC 24

Db 675 ATGTGGGTCCCGGTGTCTCTC 698

Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rml

Page 4

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RESULT 8
US-09-605-785-607
; Sequence 607, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 607
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-605-785-607

Query Match
Best Local Similarity 83.3%; Score 20; DB 4; Length 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCTT 20
Db 3 ATGTGGTCCCGGTGTCTT 22

RESULT 9
US-08-394-033-1
; Sequence 1, Application US/08394033
; Patent No. 5614372
; GENERAL INFORMATION:
; APPLICANT: Lundvall, Hans
; APPLICANT: Lovgren, Janita
; TITLE OF INVENTION: Early Detection of Prostate Cancer (CAP)
; TITLE OF INVENTION: by Employing Prostate Specific Antigen (PSA) and Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, NW, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/394,033
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FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 23635-113884
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
TELEFAX: 202-962-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-394-033-1

Query Match
Best Local Similarity 75.0%; Score 18; DB 1; Length 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGTCTC 18
Db 11 ATGTGGTCCCGGTGTCTC 28

RESULT 10
US-08-577-492-31
; Sequence 31, Application US/08577492
; Patent No. 5851784
; GENERAL INFORMATION:
; APPLICANT: Owens, Raymond John
; APPLICANT: Perry, Martin John
; APPLICANT: Lumb, Simon Mark
; TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND
; TITLE OF INVENTION: ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5851784 is
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/577,492
; FILING DATE: 22-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426227.6
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9512996.1
; FILING DATE: 26-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cherry, David A.
; REGISTRATION NUMBER: 35,099
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2153 base pairs
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TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-577-492-31

Query Match 75.0%; Score 18; DB 2; Length 2153;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTCCCGGTGCTCTCT 23  
DB 198 GGTCCCGGTGCTCTCT 215

RESULT 11  
US-09-079-630-31  
Sequence 31, Application US/09079630  
Patent No. 6291199  
GENERAL INFORMATION:  
APPLICANT: Owens, Raymond John  
APPLICANT: Perry, Martin John  
TITLE OF INVENTION: HUMAN PHOSPHODIESTERASE TYPE IVC, AND  
TITLE OF INVENTION: ITS PRODUCTION AND USE  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6291199Pis  
STREET: One Liberty Place, 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079, 630  
FILING DATE:

CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/577,492  
FILING DATE: 22-DEC-1995  
APPLICATION NUMBER: GB 9426227.6  
FILING DATE: 23-DEC-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: GB 9512996.1  
FILING DATE: 26-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Cherry, David A.

REGISTRATION NUMBER: 35,099  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2153 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-079-630-31

Query Match 75.0%; Score 18; DB 4; Length 2153;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGTCCCGGTGCTCTCT 23  
DB 198 GGTCCCGGTGCTCTCT 215

RESULT 12

US-09-042-071-19/C  
Sequence 19, Application US/09042071  
Patent No. 6294372

GENERAL INFORMATION:  
APPLICANT: Burian, Jan  
APPLICANT: Kay, William W.  
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM  
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING  
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,071  
FILING DATE: 13-MAR-1998

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 660081, 407  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1548 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-042-071-19

Query Match 73.3%; Score 17.6; DB 4; Length 1548;  
Best Local Similarity 83.3%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTGCTCTCTC 24  
DB 411 ATGTGGTCCCGGTGCTCTCTCCG 388

RESULT 13  
US-08-454-720A-38/C  
Sequence 38, Application US/08454720A  
Patent No. 5766888

GENERAL INFORMATION:  
APPLICANT: Sobol, Robert E.  
APPLICANT: Green, Mark R.  
TITLE OF INVENTION: Detection of Carcinoma Metastases by  
TITLE OF INVENTION: Nucleic Acid Amplification  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffman-La Roche, Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0L, version

Tue Nov 19 15:43:50 2002

us-09-829-004a-7.rni

Page 6

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,720A
; FILING DATE: May 31, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/357,565
; FILING DATE: December 16, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas
; REGISTRATION NUMBER: 35321
; REFERENCE/DOCKET NUMBER: 9178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1864 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-454-720A-38

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Query Match          68.3%; Score 16.4; DB 1; Length 1864;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 7 GTCCGGTGTCTCTCTC 24
DB 1189 GTCCGGTGTCTCTCTC 1172

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RESULT 14
US-08-983-075D-10
; Sequence 10 Application US/08983075D
; Patent No. 6303361
; GENERAL INFORMATION:
; APPLICANT: VIKKO, Pirkko
; TITLE OF INVENTION: HUMAN GLANDULAR KALLIKREIN-1 (HK2)
; FILE REFERENCE: 1491/44025
; CURRENT APPLICATION NUMBER: US/08/983,075D
; CURRENT FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: PCT/FI96/00382
; PRIOR FILING DATE: 1996-06-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: nucleotide sequence encoding the prepro-sequence
US-08-983-075D-10

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Query Match          66.7%; Score 16; DB 4; Length 72;
Best Local Similarity 79.2%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGTGGTCCCGGTGTCTCTC 24
DB 1 ATGTGGACCTGTCTCTCCATC 24

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RESULT 15
US-09-385-982-435/C
; Sequence 435, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II

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; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 344
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 435
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-435

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Query Match          66.7%; Score 16; DB 4; Length 558;
Best Local Similarity 79.2%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 ATGTGGTCCCGGTGTCTCTC 24
DB 237 ATTTGGTCCACCTCTCTCTC 214

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Search completed: November 19, 2002, 05:20:20
Job time : 54.0769 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:04:51 : Search time 81.2308 Seconds  
(without alignments)  
111.898 Million cell updates/sec

Title: US-09-829-004A-7  
Perfect score: 24  
Sequence: 1 atgtggccggttcttctc 24

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA.\*

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2: /cgn2\_6/ptodata/1/pubpna/PCCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
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11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	24	100.0	1709	10	US-09-755-100-4
3	24	100.0	3423	10	US-09-755-100-5
4	24	100.0	3846	10	US-09-755-100-3
5	24	100.0	4661	10	US-09-755-100-1
6	24	100.0	4661	10	US-09-755-100-2
7	20	83.3	22	10	US-09-759-143-607
8	20	83.3	22	10	US-09-780-669-607
9	20	83.3	22	10	US-09-822-827-607
10	19.2	80.0	612	10	US-09-974-300-2790
11	16.8	70.0	1484	9	US-09-764-868-429
12	16.8	70.0	2484	10	US-09-036-613-4
13	16.2	67.5	569	10	US-09-864-761-16219
14	16.2	67.5	975	9	US-09-938-842A-2277
15	16.2	67.5	33239	10	US-09-814-950-3
16	16.2	67.5	31	10	US-09-801-274-979
17	16	66.7	373	10	US-09-864-761-20503
18	16	66.7	381	10	US-09-960-352-13058
19	16	66.7	393	10	US-09-960-352-2854

20	16	66.7	432	10	US-09-960-352-12564	Sequence 12564, A
21	16	66.7	434	10	US-09-960-352-11130	Sequence 11130, A
22	16	66.7	443	10	US-09-960-352-257	Sequence 257, App
23	16	66.7	447	10	US-09-920-300A-335	Sequence 335, App
24	16	66.7	447	12	US-10-033-528-335	Sequence 335, App
25	16	66.7	450	10	US-09-960-352-4535	Sequence 4535, App
26	16	66.7	861	10	US-09-925-297-286	Sequence 286, App
27	16	66.7	871	10	US-09-956-999-7	Sequence 7, Appli
28	16	66.7	871	10	US-09-962-832-101	Sequence 101, App
29	16	66.7	871	10	US-09-880-107-2307	Sequence 2307, App
30	16	66.7	1144	10	US-09-974-300-1552	Sequence 1552, App
31	16	66.7	1261	10	US-09-755-100-6	Sequence 6, Appli
32	16	66.7	1500	10	US-09-938-642-1	Sequence 1, Appli
33	16	66.7	1678	10	US-09-925-300-153	Sequence 153, App
34	16	66.7	2044	10	US-09-925-302-348	Sequence 348, App
35	16	66.7	2169	12	US-10-044-090-347	Sequence 347, App
36	15.8	65.8	54	10	US-09-918-063-65	Sequence 65, Appl
37	15.8	65.8	54	10	US-09-918-063-67	Sequence 67, Appl
38	15.8	65.8	275	10	US-09-777-564-699	Sequence 699, App
39	15.8	65.8	319	10	US-09-777-564-1235	Sequence 1235, App
40	15.8	65.8	412	9	US-09-736-457-1047	Sequence 1047, App
41	15.8	65.8	612	10	US-09-918-063-14	Sequence 14, Appl
42	15.8	65.8	612	10	US-09-918-063-16	Sequence 16, Appl
43	15.8	65.8	612	10	US-09-918-063-29	Sequence 29, Appl
44	15.8	65.8	612	10	US-09-918-063-31	Sequence 31, Appl
45	15.8	65.8	681	10	US-09-918-063-73	Sequence 73, Appl

#### ALIGNMENTS

RESULT 1  
US-09-829-004A-7  
Sequence 7, Application US/09829004A  
Patent No. US20020132976A1  
GENERAL INFORMATION:  
APPLICANT: Chong, Pele  
APPLICANT: Pedyczak, Artur  
TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Antigen (P  
FILE REFERENCE: 11014-24  
CURRENT APPLICATION NUMBER: US/09/829,004A  
CURRENT FILING DATE: 2001-04-16  
PRIOR APPLICATION NUMBER: US 60/195,456  
PRIOR FILING DATE: 2000-04-10  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 24  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: CLP313  
US-09-829-004A-7

Query Match 100.0%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGTGTCTTCTC 24  
DB 1 ATGTGGTCCCGTGTCTTCTC 24

RESULT 2  
US-09-755-100-4  
Sequence 4, Application US/09755100  
Patent No. US20020099189A1  
GENERAL INFORMATION:  
APPLICANT: SAVITZKY, Kinnetet et al.  
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES  
FILE REFERENCE: 2786-0156P

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us-09-829-004a-7.rnpb

Page 2

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; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-4

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 1709;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
Db 1502 ATGTGGTCCCGGTTGCTTCCTC 1525

RESULT 3
US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 3423;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
Db 1502 ATGTGGTCCCGGTTGCTTCCTC 1525

RESULT 4
US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
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; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 3846;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
Db 1502 ATGTGGTCCCGGTTGCTTCCTC 1525

RESULT 5
US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match
Best Local Similarity 100.0%; Score 24; DB 10; Length 4661;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGTCCCGGTTGCTTCCTC 24
Db 1502 ATGTGGTCCCGGTTGCTTCCTC 1525

RESULT 6
US-09-755-100-2
; Sequence 2, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-755-100-2

Query Match 100.0%; Score 24; DB 10; Length 4661;  
Best Local Similarity 100.0%; Pred. No. 0.029;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCTC 24  
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DB 1502 ATGTGGGTCCCGGTGTCTCTC 1525

RESULT 7

US-09-759-143-607  
; Sequence 607, Application US/09759143  
; Patent No. US20020022248A1

; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqun  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepier, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; CURRENT FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 607  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-759-143-607

Query Match 83.3%; Score 20; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20  
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DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 8

US-09-780-669-607  
; Sequence 607, Application US/09780669  
; Patent No. US20020051977A1

; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqun  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Hepier, William  
; APPLICANT: Hural, John  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C24  
; CURRENT APPLICATION NUMBER: US/09/780,669  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 943  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 607  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-780-669-607

Query Match 83.3%; Score 20; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20  
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DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 9

US-09-822-827-607  
; Sequence 607, Application US/09822827  
; Patent No. US20020081680A1

; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.534C1  
; CURRENT APPLICATION NUMBER: US/09/822,827  
; CURRENT FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 962  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 607  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-822-827-607

Query Match 83.3%; Score 20; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGGTCCCGGTGTCTCT 20  
|||||  
DB 3 ATGTGGGTCCCGGTGTCTCT 22

RESULT 10

US-09-974-300-2790/c  
; Sequence 2790, Application US/09974300  
; Patent No. US20020146721A1

; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods for Monitoring Multiple Gene  
; FILE REFERENCE: 10085.500-US

```

APPLICANT: Tang, Y. Tom
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: SYNAPSE RELATED GLYCO PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,613
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0488 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINOS12
CLONE: 2762136
US-09-036-613-4

Query Match 70.0%; Score 16.8; DB 10; Length 2484;
Best Local Similarity 90.0%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 GTGGGTCGCCGTTGCTTCC 22
Db 586 GTGGGCCCGCGTGTTC 567

RESULT 13
US-09-864-761-16219
; Sequence 16219, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

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PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 16219  
LENGTH: 569  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC007539.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
US-09-864-761-16219

Query Match 67.5%; Score 16.2; DB 10; Length 569;  
Best Local Similarity 85.7%; Pred. No. 89;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 GTGGGTCCCGGTGCTTCCT 23  
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Db 455 GTGGGGCCAGGTGCTCCTCCT 475

RESULT 14  
US-09-938-842A-2277/c  
Sequence 2277, Application US/09938842A  
Patent No. US20020160378A1  
GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
TITLE OF INVENTION: SAME, AND METHODS OF USE  
FILE REFERENCE: SRRP1300-3  
CURRENT APPLICATION NUMBER: US/09/938, 842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 2277  
LENGTH: 975  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2277

Query Match 67.5%; Score 16.2; DB 9; Length 975;  
Best Local Similarity 85.7%; Pred. No. 95;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TGGGTCCCGGTGCTTCCTC 24  
||||| ||||||| ||||  
Db 343 TGATCCCGGTGCTTCCTC 323

RESULT 15  
US-09-814-950-3  
Sequence 3, Application US/09814950  
Patent No. US20020137130A1  
GENERAL INFORMATION:  
APPLICANT: Wei, Ming-Hui et al  
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
FILE REFERENCE: CL001174  
CURRENT APPLICATION NUMBER: US/09/814,950  
CURRENT FILING DATE: 2001-03-23  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 33239  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(33239)  
OTHER INFORMATION: n = A,T,C or G  
US-09-814-950-3

Query Match 67.5%; Score 16.2; DB 10; Length 33239;  
Best Local Similarity 85.7%; Pred. No. 14e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGTGGTCCCGGTGCTTCCTC 22  
||||| ||||||| |||||||  
Db 27025 TGTGGTCCAGGTGCTTCCTC 27045

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Job time: 90.2308 secs

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## OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 00:33:44 ; Search time 1026.35 Seconds

(without alignments)  
765.603 Million cell updates/sec

Title: US-09-829-004A-8

Perfect score: 27  
Sequence: 1 gttctgtgtcaccaccagtggtctctc 27Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

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1: gb\_ba: \*  
2: gb\_hgt: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vt: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_in: \*  
19: em\_mu: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
26: em\_ro: \*  
27: em\_sts: \*  
28: em\_un: \*  
29: em\_vt: \*  
30: em\_hgt\_hum: \*  
31: em\_hgt\_inv: \*  
32: em\_hgt\_other: \*  
33: em\_hgt\_mus: \*  
34: em\_hgt\_pln: \*  
35: em\_hgt\_rod: \*  
36: em\_hgt\_mem: \*  
37: em\_hgt\_vrt: \*  
38: em\_sy: \*  
39: em\_hgt\_hum: \*  
40: em\_hgt\_mus: \*  
41: em\_hgt\_other: \*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	27	6 AX281251	AX281251 Sequence
2	27	100.0	200	6 AR047835	AR047835 Sequence
3	27	100.0	287	9 HSPSA2	X13941 Human PSA g
4	27	100.0	569	9 S75755	S75755 PSA-Prostat
5	27	100.0	658	9 HUMPC	M21897 Human prost
6	27	100.0	708	9 HSA310937	AR153342 Sequence
7	27	100.0	711	6 AR153342	AR153342 Sequence
8	27	100.0	711	6 BD007601	BD007601 Method to
9	27	100.0	870	9 HSA459783	AJ459783 Homo sapi
10	27	100.0	876	9 HSA459782	AJ459782 Homo sapi
11	27	100.0	990	9 HSU17040	U17040 Human prost
12	27	100.0	992	6 I67863	I67863 Sequence 13
13	27	100.0	1130	9 AF335477	AF335477 Homo sapi
14	27	100.0	1350	6 AX200986	AX200986 Sequence
15	27	100.0	1350	6 AX267642	AX267642 Sequence
16	27	100.0	1415	9 HUMPA	M21895 Human prost
17	27	100.0	1446	9 HUMAPS	M2663 Homo sapien
18	27	100.0	1462	6 I67864	I67864 Sequence 14
19	27	100.0	1466	6 E32812	E32812 Primer DNA
20	27	100.0	1466	9 HSPSAR	X05332 Human mRNA
21	27	100.0	1492	9 BC005307	BC005307 Homo sapi
22	27	100.0	1514	9 MPMROS	X73560 M.mutata m
23	27	100.0	1603	9 HSA310938	AJ310938 Homo sapi
24	27	100.0	1654	9 HUMPAR	M21896 Human prost
25	27	100.0	1729	6 AR059540	AR059540 Sequence
26	27	100.0	1729	6 AR082934	AR082934 Sequence
27	27	100.0	1729	6 AX37560	AX37560 Sequence
28	27	100.0	1729	9 HSPSA	X07730 Human mRNA
29	27	100.0	1945	9 AF335478	AF335478 Homo sapi
30	27	100.0	2106	6 AX106218	AX106218 Sequence
31	27	100.0	3423	6 AX033404	AX033404 Sequence
32	27	100.0	3846	6 AX033402	AX033402 Sequence
33	27	100.0	4661	6 AX033400	AX033400 Sequence
34	27	100.0	4661	6 AX033401	AX033401 Sequence
35	27	100.0	5873	9 HSPSAG	X14810 Human prost
36	27	100.0	6153	9 HUMPSANTIG	M24543 Human DNA f
37	27	100.0	7130	6 A37262	A37262 Sequence 2
38	27	100.0	7130	6 AR167395	AR167395 Sequence
39	27	100.0	7130	9 HUMPSAA	M27274 Human prost
40	27	100.0	40458	9 AC011523	AC011523 Homo sapi
41	27	100.0	217346	2 AC027602	AC027602 Homo sapi
42	27	100.0	230000	9 AF243527	AF243527 Homo sapi
43	23.8	88.1	711	6 AR105688	AR105688 Sequence
44	23.8	88.1	711	6 AR105695	AR105695 Sequence
45	23.8	88.1	711	6 AR153341	AR153341 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS AX281251 27 bp DNA  
DEFINITION Sequence 8 from Patent WO0176622.  
ACCESSION AX281251  
VERSION AX281251.1 GI:16608507  
KEYWORDS  
ORGANISM  
SOURCE  
REFERENCE 1  
AUTHORS Pedyczak, A., Chong, P. and Sia, C.D.  
TITLE Immunogenic peptides derived from prostate-specific antigen (psa)  
and uses thereof  
JOURNAL Patent: WO 0176622-A 8 18-OCN-2001;

Pred. No. is the number of results predicted by chance to have a

Avantis Pasteur Limited (CA)  
Location/Qualifiers  
1. .27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="CIP314"

BASE COUNT 2 a 10 c 8 g 7 t

ORIGIN

Query Match 100.0%; Score 27; DB 6; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.047;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27  
Db 1 GTTCTGTGCACCCCGAGTGGTCTC 27

RESULT 2  
AR047835 200 bp DNA linear PAT 29-SEP-1999  
LOCUS  
DEFINITION Sequence 1 from patent US 5817798;  
ACCESSION AR047835  
VERSION AR047835.1 GI:5969300  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 200)  
AUTHORS Gundling, G.J.  
TITLE Rapid RNA isolation procedure in the presence of a transition metal ion  
JOURNAL Patent: US 5817798-A 1 06-OCT-1998;  
FEATURES  
LOCATION/Qualifiers  
SOURCE 1.200  
BASE COUNT 31 a 58 c 67 g 44 t

Query Match 100.0%; Score 27; DB 6; Length 200;  
Best Local Similarity 100.0%; Pred. No. 0.048;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27  
Db 120 GTTCTGTGCACCCCGAGTGGTCTC 146

RESULT 3  
HSPSA2 287 bp DNA linear PRI 24-AUG-1989  
LOCUS  
DEFINITION Human PSA gene for prostate specific antigen exon 2.  
ACCESSION X13941.1 GI:35724  
VERSION X13941.1 GI:35724  
KEYWORDS kallikrein; prostate specific antigen; PSA gene.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 287)  
AUTHORS Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE Digby, M.R.  
JOURNAL Direct Submission  
SUBMITTED (09-JAN-1989) Digby M.R., The Howard Florey Institute, Melbourne University, Parkville, Victoria 3052, Australia  
REFERENCE 2 (bases 1 to 287)  
AUTHORS Digby, M., Zhang, X.Y. and Richards, R.I.  
TITLE Human prostate specific antigen (PSA) gene: structure and linkage to the kallikrein-like gene, hK1  
JOURNAL Nucleic Acids Res. 17 (5), 2137 (1989)  
MEDLINE 89183632  
JOURNAL 2467258  
COMMENT data kindly reviewed (16-may-1989) by Digby M.R.  
FEATURES Location/Qualifiers

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1. .287  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="chromosome 19"  
/clone="CHK-2"  
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1. .107  
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108. .267  
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108. .267  
/note="prostate specific antigen (AA 16-69) (108 is 2nd base in codon) (267 is 2nd base in codon); Protein sequence is in conflict with the conceptual translation"  
/codon\_start=1  
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268. .287  
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BASE COUNT 43 a 100 c 78 g 86 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27  
Db 218 GTTCTGTGCACCCCGAGTGGTCTC 244

RESULT 4  
S75755 569 bp mRNA linear PRI 15-JUN-1995  
LOCUS  
DEFINITION PSA-prostate-specific antigen [human, breast cancer specimen, mRNA Partial, 569 nt].  
ACCESSION S75755  
VERSION S75755.1 GI:861469  
KEYWORDS  
SOURCE Homo sapiens breast cancer specimen.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 569)  
AUTHORS Eukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE Monne, M., Croce, C.M., Yu, H. and Diamandis, E.P.  
JOURNAL Molecular characterization of prostate-specific antigen messenger RNA expressed in breast tumors  
Cancer Res. 54 (24), 6344-6347 (1994)  
MEDLINE 95079406  
JOURNAL 7527295  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI g1bbsq 161505] from the original journal article.  
FEATURES  
LOCATION/Qualifiers  
SOURCE 1. .569  
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BASE COUNT      108 a      182 c      160 g      119 t
ORIGIN
LGTTCYASGWSIEPEEFLTPKKIQCVDL"

Query Match      100.0%; Score 27; DB 9; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GTTCTGTGCACCCCGAGTGGTCTC 27
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Db      198 GTTCTGTGCACCCCGAGTGGTCTC 224

RESULT 5
LOCUS      HUMPAK      658 bp      mRNA      linear      PRI 07-JAN-1995
DEFINITION Human prostate specific antigen (PA) gene, 3' end, clone PA 424.
ACCESSION M21897
VERSION M21897.1 GI:189529
KEYWORDS glycoprotein; prostate antigen; prostate-specific antigen;
          semioangelin.
SOURCE      Human prostate tumor cell line PC 82, CDNA to mRNA, clone PA 424.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 658)
AUTHORS     Riegman,P.H., Klaassen,P., van der Korp,J.A., Romijn,J.C. and
            Trapman,J.
TITLE       Molecular cloning and characterization of novel prostate antigen
            CDNA's
JOURNAL      Biochem. Biophys. Res. Commun. 155 (1), 181-188 (1988)
MEDLINE     8836297
PUBMED      2458104
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            /db_xref="GI:189530"
            /db_xref="GDB:600-119-695"
            /translation="VVFILSVTWIGAAPLISRIYGVGNECKHSQPMQVLAASRGRA
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176 bp upstream of PvuII site.

Query Match      100.0%; Score 27; DB 9; Length 658;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GTTCTGTGCACCCCGAGTGGTCTC 27
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Db      146 GTTCTGTGCACCCCGAGTGGTCTC 172

RESULT 6
LOCUS      HSAJ10937      708 bp      mRNA      linear      PRI 17-JAN-2002
DEFINITION Homo sapiens mRNA for putative preproPSA-RP2 (KLK3 gene),

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transcript 1.
ACCESSION      AJ310937
VERSION        AJ310937.1 GI:14422304
KEYWORDS       alternative splicing; HKLK3 gene; kallikrein 3; preproPSA-RP2.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1
AUTHORS        Heuze-Vourc'h,N., Leblond,Y., Olayat,S., Gauthier,F. and Courty,Y.
TITLE          Characterization of PSA-RP2, a protein related to prostate-specific
            antigen and encoded by alternative HKLK3 transcripts
JOURNAL        Eur J. Biochem. 268 (16), 4408-4413 (2001)
MEDLINE        21393944
PUBMED         11502200
REFERENCE      2 (bases 1 to 708)
AUTHORS        Courty,Y.
TITLE          Direct Submission
JOURNAL        Submitted (11-APR-2001) Courty Y., Faculte de Medecine, EMI-U 0010,
            laboratoire d'Enzymologie, 2 bis bd Tonnelie, 37032 Tours cedex,
            FRANCE
COMMENT        related accession number AJ310938;
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DEFINITION Sequence 4 from patent US 6235486.
ACCESSION      AR153342
VERSION        AR153342.1 GI:15120874
KEYWORDS

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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 711)  
AUTHORS Young,C.Y.F., Tindall,D.J. and Klee,G.G.  
TITLE Method for detection of breast cancer  
JOURNAL Patent: US 623486 A 4 22-MAY-2001;  
FEATURES Location/Qualifiers  
Source 1..711  
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BASE COUNT 148 a 208 c 206 g 149 t  
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Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 85 GTTCTGTGACCCCGAGTGGTCTC 111  
RESULT 8  
BD007601 711 bp DNA linear PAT 31-JAN-2002  
LOCUS Method for detecting metastatic prostatic cancer.  
DEFINITION BD007601  
ACCESSION BD007601 GI:18635974  
VERSION JP 2001503991-A/14.  
KEYWORDS unidentified.  
SOURCE unidentified.  
ORGANISM unclassified.  
REFERENCE 1 (bases 1 to 711)  
AUTHORS Tindall,D.J., Young,C.Y.F., McCormic,D.J., Klee,G.G., Saeedi,M.S.,  
Kumar,A., Rittenhouse,H.G. and Wolfert,R.L.  
TITLE Method for detecting metastatic prostatic cancer  
JOURNAL Patent: JP 2001503991-A 14 27-MAR-2001;  
COMMENT MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH, HYBRITTECH INC  
OS Unidentified  
PM JP 2001503991-A/14  
PD 27-MAR-2001  
PF 14-NOV-1997 JP 1998522888  
PR 14-NOV-1996 US 08/759354  
PI DONALD J TINDALL, CHARLES Y F YOUNG, DANIEL J MCCORMIC, PI  
GEORGE G KLEE,  
PI MOHAMMAD SAEED SAEDI, ABHAY KUMAR, HARRY G RITTENHOUSE, PI  
ROBERT L WOLFERT  
PC C12N15/09, C07K16/40, C12N5/10, C12N9/64, C12P21/08, C12O1/68, PC  
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Db 85 GTTCTGTGACCCCGAGTGGTCTC 111  
RESULT 9  
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LOCUS HSA459783 870 bp mRNA linear PRI 09-MAY-2002  
DEFINITION Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice  
variant 2.  
ACCESSION A1459783  
VERSION A1459783.1 GI:20520642  
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Heuze-Vourc'h,N. and Courty,Y.  
Complex alternative splicing of the hKLK3 gene coding for the  
tumour marker PSA (prostate-specific-antigen)  
Unpublished  
2 (bases 1 to 870)  
Courty,Y.  
Direct Submission  
Submitted (03-MAY-2002) Courty Y., EMI-U 0010, Laboratoire  
d'enzymologie, Universite F. Rabatelais, 2 bis bvd Tonnelier, Tours,  
37032 Cedex FRANCE  
alternative splice variant sequences: A1459782, A1459784.  
FEATURES Location/Qualifiers  
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MSLKNRFLRPDDSSHDMLRUSEPRLIDAKYWDIPROPALACTGCTGYSAGMSI  
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22..72  
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 178 GTTCTGTGACCCCGAGTGGTCTC 204  
RESULT 10  
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LOCUS Homo sapiens mRNA for prostate specific antigen (KLK3 gene), splice  
variant 1.  
DEFINITION  
ACCESSION A1459782  
VERSION A1459782.1 GI:20520640  
KEYWORDS alternative splicing; KLK3 gene; prostate specific antigen.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1

AUTHORS Heuze-Yourc'h, N. and Court'y, Y.  
TITLE Complex alternative splicing of the hKlk3 gene coding for the  
tumor marker PSA (prostate specific-antigen)  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 876)  
AUTHORS Court'y, Y.  
TITLE Direct Submission  
JOURNAL Submitted (03-MAY-2002) Court'y Y., EMI-U 0010, Laboratoire  
d'Enzymologie, Universite F. Rabelaais, 2 bis bvd Tonnelie, Tours,  
37032 cedex, FRANCE  
COMMENT alternative splice variant sequences: A459783, A459784.  
FEATURES  
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/db\_xref="taxon:9606"  
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QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
Db 178 GTTCTGTGACCCCGAGTGGTCTC 204  
RESULT 11  
HSU17040 990 bp mRNA linear PRI 07-DEC-1994  
LOCUS Human prostate specific antigen precursor mRNA, complete cds.  
DEFINITION U17040  
ACCESSION U17040  
VERSION U17040.1 GI:595945  
KEYWORDS  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.  
REFERENCE 1 (bases 1 to 990)  
AUTHORS Monne, M.M., Moreno, J.M., Mele, C.M., Mulholland, G.M. and  
Gomella, L.G.  
TITLE A Comparative Analysis of Prostate Specific Antigen Gene Sequence  
JOURNAL In Benign and Malignant Prostate Tissue  
REFERENCE Unpublished  
AUTHORS Moreno, J.M.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-1994) Jose M J G Moreno, Urology, Thomas  
Jefferson University Hospital, 1025 Walnut Street, Philadelphia, PA  
19107, USA  
FEATURES Location/Qualifiers

source  
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EPEFLTPKLCQVDLHVISNDVCAQVHPQVTKPMLCAGRWTKGKSTCSGDSGSPV  
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misc\_feature 93..113  
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 12  
167863 992 bp DNA linear PAT 04-FEB-1998  
LOCUS Sequence 13 from patent US 5674682.  
DEFINITION 167863  
ACCESSION 167863  
VERSION 167863.1 GI:2829985  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 992)  
AUTHORS Croce, C., Gomella, L., Mulholland, S., Grant, J., Moreno, J.G. and  
Fischer, R.  
TITLE Nucleic acid primers for detecting micrometastasis of prostate  
cancer  
JOURNAL Patent: US 5674682-A 13 07-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..992  
/organism="unknown"  
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QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
Db 200 GTTCTGTGACCCCGAGTGGTCTC 226  
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AF335477 1130 bp mRNA linear PRI 13-MAY-2002  
LOCUS Homo sapiens prostate-specific antigen variant 1 mRNA, complete  
DEFINITION AF335477  
ACCESSION AF335477  
VERSION AF335477.1 GI:18478569  
KEYWORDS

SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 1130)  
David, A., Mabsesh, N., Azar, I., Bilton, S., Engel, S., Bernstein, J.,  
Romano, J., Avigor, Y., Waks, T., Eshhar, Z., Langer, S.Z.,  
Lifschitz-Mercer, B., Matzkin, H., Rotman, G., Toporik, A., Savitsky, K.  
and Mintz, L.  
TITLE Unusual alternative splicing within the human kallikrein genes KLK2  
and KLK3 gives rise to novel prostate-specific proteins  
JOURNAL J. Biol. Chem. 277 (20), 18084-18090 (2002)  
MEDLINE 22001285  
PUBMED 11834722  
AUTHORS 2 (bases 1 to 1130)  
David, A., Engel, S., Azar, I., Bernstein, J., Rotman, G., Savitsky, K.  
and Mintz, L.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-2001) Compugen Ltd., 72 Pinchas Rosen, Tel Aviv  
69512, Israel  
FEATURES  
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/db\_xref="GI:18478570"  
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DB 621 GTTCTGTGCACCCCGAGTGGTCTC 647  
RESULT 14  
AX200986 1350 bp DNA linear PAT 29-AUG-2001  
LOCUS Sequence 616 from Patent W00151633.  
DEFINITION AX200986  
ACCESSION AX200986  
VERSION AX200986.1 GI:15390813  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1350)  
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W.,  
Stolk, J.A., Skeiky, Y.A., Wang, A., and Mesgher, M.J.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: WO 0151633-A 616 19-JUL-2001;  
CORIXA CORPORATION (US)  
FEATURES  
Source Location/Qualifiers  
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DB 778 GTTCTGTGCACCCCGAGTGGTCTC 804  
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AX267642 1350 bp DNA linear PAT 26-OCT-2001  
LOCUS Sequence 616 from Patent W00173032.  
DEFINITION AX267642  
ACCESSION AX267642  
VERSION AX267642.1 GI:16516315  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,  
Kalos, M.D., Fanger, G.R., Retter, M.W., Stolk, J.A., Day, C.H.,  
Vedvick, I.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A., Hepler, W.T.  
and Henderson, R.A.  
TITLE Compositions and methods for the therapy and diagnosis of prostate  
cancer  
JOURNAL Patent: WO 0173032-A 616 04-OCT-2001;  
CORIXA CORPORATION (US)  
FEATURES  
Source Location/Qualifiers  
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DB 778 GTTCTGTGCACCCCGAGTGGTCTC 804  
Search completed: November 19, 2002, 04:02:54  
Job time : 1028.68 secs

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	27	100.0	178	24	ABA01120
4	27	100.0	200	19	AAV60379
5	27	100.0	208	18	AAT92975
6	27	100.0	517	21	AAA61482
7	27	100.0	517	22	AAH41845
8	27	100.0	711	20	AAK08947
9	27	100.0	744	24	ABK86205

10	27	100.0	841	23	ABV25078	Human prostate exp
11	27	100.0	990	21	AAZ47134	Human prostate-spe
12	27	100.0	992	18	AAT91054	Human prostate-spe
13	27	100.0	992	20	AAK99846	Prostate specific
14	27	100.0	1040	22	AAH99720	Human prostate enco
15	27	100.0	1066	21	AAC03740	Human secreted pro
16	27	100.0	1329	23	ABV23473	Human prostate exp
17	27	100.0	1329	23	ABV29201	Human prostate exp
18	27	100.0	1350	22	AAK63953	Human CDNA encodin
19	27	100.0	1350	22	AAH93860	p703p and PSA fusi
20	27	100.0	1350	24	ABU93524	Human p703p/PSA fu
21	27	100.0	1445	19	AAV32497	Prostate specific
22	27	100.0	1462	18	AAT91055	Human prostate spe
23	27	100.0	1462	18	AAK99847	Prostate specific
24	27	100.0	1466	19	AAV32496	Prostate specific
25	27	100.0	1466	21	AAH11711	Human prostate-spe
26	27	100.0	1728	17	AAT35867	Prostate-specific
27	27	100.0	1729	16	AAT04864	Prostate-specific
28	27	100.0	1729	24	ABU69732	Prostate cancer re
29	27	100.0	2106	22	AAK69598	Human WT1/PSA fusi
30	27	100.0	3423	21	AAA64171	DNA encoding a hum
31	27	100.0	3846	21	AAH64169	DNA encoding a hum
32	27	100.0	4661	21	AAA64167	DNA encoding a hum
33	27	100.0	4661	21	AAA64168	DNA encoding a hum
34	27	100.0	5873	18	AAT61701	Human prostatic sp
35	25.4	94.1	1866	23	ABV23503	Human prostate exp
36	25.4	94.1	1866	23	ABV24768	Human prostate exp
37	25.4	94.1	1866	23	ABV29105	Human prostate exp
38	25.4	94.1	1866	23	ABV29331	Human prostate exp
39	24.4	90.4	151	23	ABV38196	Human prostate exp
40	23.8	88.1	163	23	ABV37921	Human prostate exp
41	23.8	88.1	233	23	ABV45098	Human prostate exp
42	23.8	88.1	275	21	AAC72139	Single nucleotide
43	23.8	88.1	385	21	AAK04575	Human secreted pro
44	23.8	88.1	441	23	AAV15240	Human prostate exp
45	23.8	88.1	711	19	AAV70339	Prostate-specific

#### ALIGNMENTS

RESULT 1	
ID	AAD21362 standard; DNA; 27 BP.
AC	AAD21362;
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DT	28-JAN-2002 (first entry)
XX	
DE	Prostate specific antigen (PSA) derived peptide, CLP314 encoding DNA.
XX	
KW	Prostate-specific antigen; PSA; immunogenic peptide; immune response;
KW	therapy; cancer; prostate cancer; tumour metastasis; prophylaxis; ds.
XX	
OS	Unidentified.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..27
FT	/*tag-a
FT	/product= "PSA derived peptide, CLP314"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	
PN	WO200176622-A2.
XX	
PD	18-OCT-2001.
XX	
PF	10-APR-2001; 2001WO-CA00473.
XX	
PR	10-APR-2000; 2000US-195456P.
XX	
PA	(AVENT ) AVENTIS PASTEUR LTD.
XX	

PI Pedyczak A, Chong P, Sia CDY;  
 XX WPI: 2001-663015/76.  
 DR P-PSDB; AAE13024.  
 XX  
 XX  
 PT New polypeptide, useful for treating cancers such as prostate cancer,  
 PT comprises prostate-specific antigen derived peptide -  
 PS Claim 7; Page 28; 41pp; English.  
 XX  
 XX The patent discloses immunogenic peptides of prostate-specific antigen  
 CC (PSA) and nucleic acids encoding them. The peptides of the invention  
 CC are used to prepare a medicament to elicit an immune response in an  
 CC animal. They are used to treat cancer such as prostate cancer and  
 CC tumour metastasis. They are also useful for prophylaxis, for  
 CC preparing monoclonal or polyclonal antibodies, and in conventional  
 CC techniques of immunology, molecular biology, cell biology and  
 CC recombinant DNA technology. The present sequence is a DNA encoding  
 CC PSA derived peptide, CLP314.  
 XX  
 SQ Sequence 27 BP; 2 A; 10 C; 8 G; 7 T; 0 other;  
 Query Match 100.0%; Score 27; DB:22; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.023; 0; Mismatches 0; Gaps 0;  
 Matches 27; Conservative 0; Indels 0; Gaps 0;  
 OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27  
 DB 1 GTTCTGTGTCACCCCGAGTGGTCTC 27  
 RESULT 2  
 ABA92483  
 ID ABA92483 standard; DNA; 178 BP.  
 XX  
 AC ABA92483;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE DNA oligonucleotide sequence SEQ ID NO:6.  
 XX  
 KM Detection; nucleic acid synthesis; identification; cancer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183817-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 25-APR-2001; 2001WO-JP03572.  
 XX  
 PR 01-MAY-2000; 2000JP-0132667.  
 XX  
 PA (EIKE ) EIKEN KAGAKU KK.  
 XX  
 PI Mori Y, Nagamine K;  
 XX  
 DR WPI: 2002-075170/10.  
 XX  
 PT Detecting the product of an enzyme-based nucleic acid synthesizing  
 PT reaction, useful in gene analysis, diagnosis of cancer and other  
 PT diseases, and in identifying bacteria, comprises the formation of an  
 PT insoluble substance -  
 PS Example 4; Page 18; 44pp; Japanese.  
 XX  
 XX The present invention describes a method for detecting the occurrence of  
 CC a nucleic acid synthesizing reaction during the synthesis of a nucleic  
 CC acid with an enzyme. The method comprises the use of an insoluble  
 CC substance formed in the reaction as an indication. The method can be  
 CC used for detecting the presence or absence of a nucleic acid synthesizing  
 CC reaction (especially a nucleic acid amplification reaction). The method  
 CC is useful in gene analysis, diagnosis of cancer and other diseases, and

CC in identifying bacteria. The present sequence represents an  
 CC oligonucleotide used in the exemplification of the present invention.  
 XX  
 SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 other;  
 Query Match 100.0%; Score 27; DB 24; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27  
 DB 39 GTTCTGTGTCACCCCGAGTGGTCTC 65  
 RESULT 3  
 ABA01120  
 ID ABA01120 standard; DNA; 178 BP.  
 XX  
 AC ABA01120;  
 XX  
 DT 06-FEB-2002 (first entry)  
 XX  
 DE Human PSA nucleotide sequence.  
 XX  
 KM Human; nucleic acid synthesis; complementary chain synthesis; diagnosis;  
 KM ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177317-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-JP02771.  
 XX  
 PR 07-APR-2000; 2000JP-0111939.  
 XX  
 PA (EIKE ) EIKEN KAGAKU KK.  
 XX  
 PI Notomi T, Nagamine K;  
 XX  
 DR WPI: 2002-010907/01.  
 XX  
 PT Isothermal amplification of nucleic acids using double-stranded nucleic  
 PT acid as template to establish complementary chain synthesis reaction  
 PT from primer enabling base pairing in domain to be annealed, useful e.g.  
 PT in gene diagnosis -  
 PS Example 1; Page 63; 75pp; Japanese.  
 XX  
 XX The invention relates to a method for synthesizing a nucleic acid using  
 CC a double-stranded nucleic acid as template and incubating under  
 CC conditions allowing the establishment of a complementary chain synthesis  
 CC reaction. The method uses an arbitrary primer to initiate the  
 CC complementary chain synthesis reaction. The method is particularly  
 CC useful in gene and disease diagnosis. It is a highly efficient and  
 CC reaction specific method in which no temperature variation is required.  
 CC The present sequence is used in an example illustrating the invention.  
 XX  
 SQ Sequence 178 BP; 33 A; 56 C; 50 G; 39 T; 0 other;  
 Query Match 100.0%; Score 27; DB 24; Length 178;  
 Best Local Similarity 100.0%; Pred. No. 0.034;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27  
 DB 39 GTTCTGTGTCACCCCGAGTGGTCTC 65  
 RESULT 4  
 AAV60379  
 ID AAV60379 standard; mRNA; 200 BP.



```
XX AC AAV60379;
XX XX
XX DT 07-DEC-1998 (first entry)
XX DE mRNA target sequence from exons 2 and 3 of PSA gene.
XX KM mRNA target sequence; prostate specific antigen; PSA; RNA purification;
XX KM ds.
XX OS Homo sapiens.
XX PN US5817798-A.
XX PD 06-OCT-1998.
XX PF 17-SEP-1997; 97US-0931981.
XX PR 17-SEP-1997; 97US-0931981.
XX PA (ABBO ) ABBOTT LAB.
XX PI Gundling GJ;
XX DR WPI; 1998-556473/47.
XX PT Purification of RNA, used for nucleic acid amplification and disease
XX PT detection - by precipitating other sample components with transition
XX PT metal ions, separating and collecting the purified RNA
XX PS Example 5; Columns 9-10; 6pp; English.
XX XX
XX CC The present sequence represents a mRNA target sequence from exons 2 and 3
XX CC of the prostate specific antigen (PSA) gene. The sequence is used to
XX CC exemplify the invention. The specification describes a method for
XX CC purifying RNA. The method comprises contacting a test sample with
XX CC polyvalent transition metal ions to form a precipitant and a supernatant,
XX CC separating the precipitant from the supernatant, and collecting the
XX CC supernatant to obtain a purified solution of total RNA. The RNA is
XX CC used for nucleic acid amplification and disease detection.
XX SQ Sequence 200 BP; 31 A; 58 C; 67 G; 44 T; 0 other;
XX
XX Query Match 100.0%; Score 27; DB 19; Length 200;
XX Best Local Similarity 100.0%; Pred. No. 0.035;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
XX ||||||||||||||||||||||||
XX DB 120 GTTCTGTGCACCCCGAGTGGTCTC 146
XX
XX RESULT 5
XX AAT92975
XX ID AAT92975 standard; cDNA; 208 BP.
XX XX
XX AC AAT92975;
XX XX
XX DT 24-APR-1998 (first entry)
XX DE cDNA for prostate specific antigen (PSA).
XX XX
XX KM Diagnosis; prostate cancer; prostate specific antigen; PSA;
XX KM metastatic prostate cancer; prostate cell; secondary tumour;
XX KM bone metastatic anchoring; ss.
XX XX
XX OS Homo sapiens.
XX PN WO9739139-A1.
XX PD 23-OCT-1997.
XX PF 16-APR-1997; 97WO-US06497.
```

```
XX PR 16-APR-1996; 96US-0015765.
XX XX
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Robbins DJ;
XX DR WPI; 1997-526473/48.
XX XX
XX PT Monitoring or diagnosis of prostate cancer - by detecting
XX PT prostate-specific antigen mRNA using specific primers
XX PS Disclosure; Page 16; 25pp; English.
XX XX
XX CC cDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
XX CC The detection of PSA mRNA in peripheral blood is associated with
XX CC metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
XX CC indicates that prostate cells are circulating in the blood and confirms
XX CC diagnosis of cancer. Circulating prostate cells also indicate a risk of a
XX CC secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
XX CC after prostatectomy or radiotherapy indicates a risk that the prostate
XX CC cancer has spread and that the surgery and radiotherapy was not
XX CC effective. PCR primers AAT92971-73 were used for the monitoring and
XX CC diagnosis of patients with prostate cancer. The method comprises the
XX CC detection of PSA mRNA by reverse transcriptase polymerase chain reaction
XX CC (RT-PCR).
XX SQ Sequence 208 BP; 29 A; 62 C; 73 G; 44 T; 0 other;
XX
XX Query Match 100.0%; Score 27; DB 18; Length 208;
XX Best Local Similarity 100.0%; Pred. No. 0.035;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
XX ||||||||||||||||||||||||
XX DB 133 GTTCTGTGCACCCCGAGTGGTCTC 159
XX
XX RESULT 6
XX AAA61482
XX ID AAA61482 standard; DNA; 517 BP.
XX XX
XX AC AAA61482;
XX XX
XX DT 23-OCT-2000 (first entry)
XX DE Prostate specific antigen gene fragment.
XX XX
XX KM Isothermal DNA amplification; nucleic acid synthesis; detection;
XX KM PSA gene template; prostate specific antigen; human; ds.
XX XX
XX OS Homo sapiens.
XX PN WO200028082-A1.
XX PD 18-MAY-2000.
XX PF 08-NOV-1999; 99WO-JP06213.
XX PR 09-NOV-1998; 98JP-0317476.
XX PA (EIKE ) EIKEN KAGAKU KK.
XX PI Notomi T, Hase T;
XX DR WPI; 2000-376587/32.
XX XX
XX PT Nucleic acid synthesis using primer containing a sequence identical to
XX PT one on the template for isothermal amplification using simple reagents
XX PS Example 8; Fig 17; 95pp; Japanese.
XX XX
```

CC The invention relates to a novel method of isothermal DNA amplification.  
 CC A region is produced at the 3' end of a target sequence which contains  
 CC sub-sequences designated F1, F2C and F1C, where F1C is the complement of  
 CC F1. A loop is formed by annealing of F1 to its complementary sequence  
 CC F1C, and a primer containing a sub-sequence F2 (complementary to F2C) at  
 CC its 3' end is annealed to the template. The complementary strand to the  
 CC template is synthesized using a DNA polymerase, and the process is  
 CC repeated using sub-sequences at the 3' end of the complementary strand  
 CC designated R1, R2C and R1C, using a primer containing R2 at its 3' end.  
 CC The invention also encompasses primers for the method of the invention,  
 CC and methods for the detection of a nucleic acid sequence in a sample  
 CC using a labeled probe containing a sequence complementary to the loop  
 CC region of the target sequence. The method of the invention provides  
 CC an efficient and highly specific method for isothermal amplification  
 CC of a target nucleic acid sequence using a simple reagent mixture.  
 CC The present sequence represents a prostate specific antigen (PSA)  
 CC gene fragment used as a template for the method of the invention.  
 XX

Sequence 517 BP; 94 A; 163 C; 151 G; 109 T; 0 other;  
 Query Match 100.0%; Score 27; DB 21; Length 517;  
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGCACCCCACTGGTCTCTC 27  
 |||||||||||||||||||||||||  
 Db 181 GTTCTGTGCACCCCACTGGTCTCTC 207

RESULT 7  
 ID AAH41845 standard; DNA; 517 BP.  
 AC AAH41845;  
 DT 30-AUG-2001 (first entry)  
 DE Prostate specific antigen related nucleotide sequence.  
 DE Prostate specific antigen; nucleic acid synthesis; detection; ds.  
 OS Unidentified.  
 OS WO200134790-A1.  
 PN 17-MAY-2001.  
 PD 28-MAR-2000; 2000WO-JP01919.  
 PF 08-NOV-1999; 99WO-JP06213.  
 PR (EIKE) EIKEN KAGAKU KK.  
 PA Notomi T, Hase T;  
 PI WPI: 2001-343603/36.  
 DR WPI: 2001-343603/36.  
 XX Synthesizing nucleic acids -  
 PT  
 PS Example 8; Fig 17; 96pp; Japanese.  
 XX The present invention describes a new method for synthesizing nucleic  
 CC acids comprising: (a) preparing a nucleic acid, with an F2c region, able  
 CC to form a loop by annealing the F1 region of the 3' end to the F1c  
 CC region on the same chain; (b) synthesis of a complementary chain using  
 CC the 3' end of F1 as the starting point; (c) replacing the complementary  
 CC chain by annealing an oligonucleotide containing F2' (complementary to  
 CC F2c) at its 3' end and using it as a starting point for complementary  
 CC chain synthesis by a polymerase; and (d) replacing the chain synthesised  
 CC in step c by annealing a polynucleotide containing a region  
 CC complementary to a part of the chain and using its 3' end as the  
 CC starting point. Also described are: (1) a kit for synthesizing nucleic  
 CC acids; and (2) a kit for detecting target base sequences. The present

CC sequence represents a prostate specific antigen related nucleotide  
 CC sequence, which is used in an example from the present invention.  
 XX

Sequence 517 BP; 94 A; 163 C; 151 G; 109 T; 0 other;  
 Query Match 100.0%; Score 27; DB 22; Length 517;  
 Best Local Similarity 100.0%; Pred. No. 0.038; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGCACCCCACTGGTCTCTC 27  
 |||||||||||||||||||||||||  
 Db 181 GTTCTGTGCACCCCACTGGTCTCTC 207

RESULT 8  
 ID AAX08947 standard; cDNA; 711 BP.  
 AC AAX08947;  
 DT 27-APR-1999 (first entry)  
 DE Human prostate specific antigen (PSA) gene.  
 DE Human kallikrein 2; hk2; breast cancer; diagnosis; detection;  
 KW treatment; monitoring; prostate specific antigen; PSA; ds.  
 XX Homo sapiens.

Key Location/Qualifiers  
 FT CDS 1..711  
 FT /tag= a  
 FT /label= Prostate-specific\_antigen

WO9859073-A1.  
 PD 30-DEC-1998.  
 PF 19-JUN-1998; 98WO-US12840.  
 PR 20-JUN-1997; 97US-0050963.  
 PA (KLEE/) KLEE G. G.  
 PA (MAYO-) MAYO FOUNDATION.  
 PA (TIND/) TINDALL D J.  
 PA (YOUN/) YOUNG C Y F.  
 PI Klee GG, Tindall DJ, Young CYF;  
 DR WPI: 1999-105632/09.  
 DR P-PSDB; AAW96187.  
 PT Use of human kallikrein 2 - as a marker for developing products for  
 CC the diagnosis, prognosis, monitoring and treatment of breast cancer  
 PS Disclosure: Page 34-35; 67pp; English.  
 XX Human kallikrein 2 (hk2) is expressed at elevated levels relative to  
 CC the prostate cancer antigen, prostate specific antigen (PSA) by  
 CC breast cancer cells when stimulated by androgens. Detecting levels  
 CC of hk2 may provide a simple diagnostic tool for detecting or  
 CC determining breast cancer. Detecting hk2 is achieved by producing  
 CC an hk2 DNA from hk2 RNA by reverse transcription. The hk2 DNA  
 CC obtained is then amplified by PCR and detected using probes.  
 CC Determination of breast cancer may also be determined by exposing  
 CC the hk2 polypeptide to an agent which binds to it and then detecting  
 CC the binary complex formed. The amount of complex formed correlates  
 CC directly to the presence of breast cancer in the human individual.  
 CC The methods can be used in the diagnosis, treatment and/or  
 CC monitoring of the progression or remission of breast cancer and/or  
 CC monitoring hk2 levels.  
 XX Sequence 711 BP; 148 A; 208 C; 206 G; 149 T; 0 other;

Query Match 100.0%; Score 27; DB 20; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
 ||||||||||||||||||  
 DB 85 GTTCTGTCACCCCGAGTGGTCCTC 111

RESULT 9  
 ABRK6205  
 ID ABRK6205 standard; cDNA; 744 BP.

XX AC ABRK6205;

XX DT 24-SEP-2002 (first entry)

XX DE cDNA encoding human prostate specific antigen (PSA) variant.

XX KM Human: prostate specific antigen; PSA; cytosolic; antiviral;  
 KM Immunostimulant; cell-mediated immune response; tumour; breast cancer;  
 KM Virus infection; prostate cancer; colorectal cancer; pancreatic cancer;  
 KM Lymphoma; leukemia; hepatitis; lentivirus; herpesvirus;  
 KM human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.

XX OS Homo sapiens.

XX PH key Location/Qualifiers  
 FT CDS 7..744  
 FT /\*tag- a  
 FT /product- "Prostate specific antigen (PSA) variant  
 FT with signal sequence deleted"

XX PN WO200240059-A2.

XX PD 23-MAY-2002.

XX PF 01-NOV-2001; 2001MO-US45626.

XX PR 01-NOV-2000; 2000US-0704232.

XX PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.  
 PA (MNC/) MINCHEFF M S.  
 PA (LOUK/) LOUKINOV D I.  
 PA (ZOUB/) ZOUBAK S.

XX PI Mincheff MS, Loukinov DI, Zoubak S;

XX DR WPI: 2002-527524/56.

XX DR P-PSDB: AAU98921.

XX PT Inducing a cell-mediated immune response against a target antigen,  
 PT reducing undesired cells and stimulating presentation of an antigen by  
 PT a cell, comprises administering a polynucleotide encoding a variant of  
 PT an antigen -

XX PS Disclosure: Page 121-122; 146pp; English.

XX CC The invention relates to a method of inducing a cell-mediated immune  
 CC response against a cell comprising a target antigen (I) in a subject,  
 CC treating a subject having undesired cells, for example tumour cells,  
 CC or virally infected cells (C), reducing the number of (C) in a subject,  
 CC and stimulating presentation of (I) by a cell. This is done by  
 CC administering a polynucleotide (II) encoding a variant of (I), so that  
 CC (II) expressed in a cell and cell-mediated immune response is induced.  
 CC The method can be used to treat prostate cancer, breast cancer,  
 CC colorectal cancer and pancreatic cancer, as well as lymphomas and  
 CC leukemias. The method is also useful in treating chronic viral  
 CC infections such as those caused by hepatitis viruses, lentiviruses  
 CC (including human immunodeficiency virus (HIV)), herpesviruses and the  
 CC flaviviruses and pestiviruses. The present sequence represents the coding  
 CC sequence of human prostate specific antigen (PSA) variant which

CC has the signal sequence deleted, used as a target antigen in the method  
 CC of the invention.

XX SQ Sequence 744 BP; 153 A; 222 C; 213 G; 156 T; 0 other;

Query Match 100.0%; Score 27; DB 24; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 0.039;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
 ||||||||||||||||||  
 DB 115 GTTCTGTCACCCCGAGTGGTCCTC 141

RESULT 10  
 ABV25078  
 ID ABV25078 standard; cDNA; 841 BP.

XX AC ABV25078;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 25069.

XX KM Human: prostate cancer; cytosolic; carcinogen; pharmacodynamic marker;  
 KM pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001MO-US05171.

XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX DR WPI: 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer -  
 XX

XX PS Claim 1; Page 4874; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for:

XX CC (a) assessing whether a patient is afflicted with prostate cancer;  
 CC (b) monitoring the progression of prostate cancer in a patient;  
 CC (c) assessing the efficacy of a test compound to inhibit prostate  
 CC cancer in a patient;  
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
 CC in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound;  
 CC (g) determining whether prostate cancer has metastasized in a patient;  
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
 CC patient;  
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 841 BP; 144 A; 262 C; 262 G; 173 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 841;



```

XX 07-OCT-1997.
PD 29-OCT-1992: 92US-0973322.
XX 15-DEC-1994: 94US-0358782.
XX 29-OCT-1992: 92US-0973322.
PR 23-AUG-1994: 94US-0294611.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Croce C, Fischer R, Gomella L, Moreno JG, Mulholland SG;
XX WPI; 1997-502328/46.
XX
XX Oligonucleotide primers specific for prostate specific antigen -
XX used for the diagnosis of prostate cancer micro-metastasis
XX
XX Example 7; Fig 2; 18pp; English.
XX
CC This DNA sequence comprises a 992-bp human prostate specific
CC antigen (PSA) cDNA PCR fragment. New oligonucleotide primers
CC (AAAT1044-53) are designed to amplify the PSA gene but not the human
CC glandular kallikrein gene, which has 75-85% homology to the PSA
CC gene. The primers can be used for diagnosis of prostate cancer
CC micrometastasis. A claimed diagnostic kit for detecting prostate
CC cancer comprises a pair of primers, where one of the primers is
CC selected from those given in AAAT1044-53, and a means for visualising
CC amplified DNA (ethidium bromide stain, 32p or biotin). The
CC invention also includes a method of detecting cells which express
CC prostate cancer specific sequences by detecting the presence of
CC nucleic acids specific for prostate cancer or a signal specific for
CC prostate cancer.
XX
SQ Sequence 992 BP: 210 A; 291 C; 272 G; 217 T; 2 other:

```

Query Match 100.0%; Score 27; DB 18; Length 992;  
 Best Local Similarity 100.0%; Pred. No. 0.04;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
    ||||||||||||||||||||
DB 200 GTTCTGTGTCACCCCGAGTGGTCTC 226

```

RESULT 13  
 AAAT9846  
 ID AAAT9846 standard; DNA: 992 BP.  
 XX  
 AC AAAT9846:  
 XX  
 XX 30-SEP-1999 (first entry)  
 XX  
 XX Prostate specific antigen PCR fragment.  
 DE  
 XX Prostate specific antigen; PSA; D1 stage prostate cancer;  
 KW D2 stage prostate cancer; D3 stage prostate cancer; human; diagnosis;  
 KW glandular kallikrein gene; micrometastasis; detection; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN US5939258-A.  
 XX  
 PD 17-AUG-1999.  
 XX  
 XX 12-DEC-1996: 96US-0764527.  
 PF  
 XX 15-DEC-1994: 94US-0358782.  
 PR 29-OCT-1992: 92US-0973322.  
 PR 23-AUG-1994: 94US-0294611.  
 PR 12-DEC-1996: 96US-0764527.  
 XX  
 XX (UYJE-) UNIV JEFFERSON THOMAS.

```

XX Croce C, Fischer R, Gomella L, Moreno JG, Mulholland SG;
XX WPI; 1999-468401/39.
XX
XX Detecting micrometastasis of prostate cancer
XX
XX Disclosure; Fig 2; 20pp; English.
XX
CC This sequence is a fragment of the human prostate specific antigen
CC (PSA). The invention relates to a method of detecting prostate cancer
CC micrometastasis in a patient having stage D1, D2, or D3 prostate cancer,
CC comprising: (1) obtaining a sample nucleic acid from a patient tissue;
CC (2) amplifying nucleic acids specific for prostate cancer or amplifying a
CC signal generated by hybridisation of a probe specific to a prostate
CC specific nucleic acid in the sample, comprising hybridisation to at least
CC 1 prostate cancer specific primer which is complementary to a prostate
CC cancer specific gene which does not hybridise to the human glandular
CC kallikrein gene; and (3) detecting the presence of the amplified nucleic
CC acids or the amplified signal where the presence of the amplified nucleic
CC acids or signal indicates micrometastasis of prostate cancer. The method
CC is useful for detecting micrometastasis of prostate cancer. The method
CC allows the detection of a low concentration of cells.
XX
SQ Sequence 992 BP: 210 A; 291 C; 272 G; 217 T; 2 other:

```

Query Match 100.0%; Score 27; DB 20; Length 992;  
 Best Local Similarity 100.0%; Pred. No. 0.04;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GTTCTGTGTCACCCCGAGTGGTCTC 27
    ||||||||||||||||||||
DB 200 GTTCTGTGTCACCCCGAGTGGTCTC 226

```

RESULT 14  
 AAAT9720  
 ID AAAT9720 standard; cDNA: 1040 BP.  
 XX  
 AC AAAT9720:  
 XX  
 XX 16-OCT-2001 (first entry)  
 XX  
 XX Human protein encoding cDNA sequence SEQ ID NO:555.  
 DE  
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antirheumatic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; viricide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;  
 KW antiagregant; haemostatic; vulnery; antilucer; osteopathic; eczema;  
 KW dermatological; antiallergic; antistimatic; antidiabetic; cyrostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200153455-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 22-DEC-2000: 2000WO-US35017.  
 PF  
 XX 23-DEC-1999: 99US-0471275.  
 PR 21-JAN-2000: 2000US-048725.  
 PR 25-APR-2000: 2000US-0552317.  
 XX

```

PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-457603/49.
XX P-PSDB: AAM25779.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PS treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX Claim 1: Page 604-605; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antineumatic;
CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antinaemic; antiagregant; haemostatic; vulnertary;
CC antidiabetic; cytostatic; neuroprotective; antidiabetic; nootropic;
CC antiparinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 1040 BP; 194 A; 287 C; 302 G; 257 T; 0 other;
Query Match 100.0%; Score 27; DB 22; Length 1040;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGTCACCCCAAGTGGTCTC 27
DB 190 GTTCTGTGTCACCCCAAGTGGTCTC 216

```

```

DR P-PSDB: AAC03734.
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1: SEQ ID 3738; 71pp + CD-ROM; English.
XX
PS The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. An ORF has been identified within the
XX sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX derived from 30 different tissues. EST sequences usually correspond
XX mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX well suited for isolating cDNA sequences derived from the 5' ends of
XX mRNAs and even in those cases where longer cDNA sequences have been
XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX cDNAs with intact 5' ends and can therefore be used to obtain full length
XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX gene therapy and chromosome mapping procedures. They are used to obtain
XX upstream regulatory sequences and to design expression and secretion
XX vectors.
XX
SQ Sequence 1066 BP; 230 A; 283 C; 310 G; 241 T; 2 other;
Query Match 100.0%; Score 27; DB 21; Length 1066;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCTGTGTCACCCCAAGTGGTCTC 27
DB 199 GTTCTGTGTCACCCCAAGTGGTCTC 225

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Search completed: November 19, 2002, 03:06:38  
Job time : 193.769 secs

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RESULT 15
AAC03740
ID AAC03740 standard; cDNA; 1066 BP.
XX
AC AAC03740;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 3738.
XX
KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PE 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
FA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.

```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:43:19 : Search time 1542.46 Seconds  
(without alignments)  
283.494 Million cell updates/sec

Title: US-09-829-004a-8

Perfect score: 27  
Sequence: 1 gtctgtgtcaccaccagtggtctctc 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estclu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	316	9	AA593245
2	27	100.0	336	9	AA506459
3	27	100.0	371	9	AA503943
4	27	100.0	377	9	AA603297
5	27	100.0	397	9	AA573604
6	27	100.0	435	9	AA177005

Result No.	Score	Query Match	Length	DB ID	Description
7	27	100.0	453	9	AA533652
8	27	100.0	454	9	AT685510
9	27	100.0	465	13	BI046475
10	27	100.0	470	9	AT525128
11	27	100.0	484	9	AA603529
12	27	100.0	485	9	AA573575
13	27	100.0	495	12	BE840533
14	27	100.0	505	12	BE840441
15	27	100.0	523	9	AA639901
16	27	100.0	548	9	AA578576
17	27	100.0	552	9	BE840701
18	27	100.0	572	12	BE840537
19	27	100.0	591	12	BE679591
20	27	100.0	610	9	AT557591
21	27	100.0	638	12	BE679511
22	27	100.0	662	9	AT525089
23	27	100.0	724	12	BE964653
24	27	100.0	732	9	AT547309
25	27	100.0	737	9	AT547285
26	27	100.0	738	12	BE679168
27	27	100.0	748	12	BE973983
28	27	100.0	756	12	BE676011
29	27	100.0	770	12	BE675749
30	27	100.0	784	12	BE678386
31	27	100.0	794	12	BE675511
32	27	100.0	796	12	BE674927
33	27	100.0	797	12	BE675142
34	27	100.0	797	12	BE679394
35	27	100.0	813	12	BE681507
36	27	100.0	825	12	BE677556
37	27	100.0	828	12	BE678076
38	27	100.0	841	12	BE673766
39	27	100.0	843	12	BE675323
40	27	100.0	848	12	BE673777
41	27	100.0	849	12	BE673243
42	27	100.0	859	12	BE675660
43	27	100.0	860	12	BE675331
44	27	100.0	866	12	BE965220
45	27	100.0	868	12	BE673807

## ALIGNMENTS

RESULT 1  
LOCUS AA593245  
DEFINITION n07e10.s1 NCI CGAP Pr4.1 Homo sapiens CDNA clone IMAGE:1077066  
similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);  
mRNA sequence.  
ACCESSION AA593245  
VERSION AA593245.1 GI:2409007  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 316)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: W. Maxton Linehan, M.D., Rodrigo Chuagui, M.D.,  
Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Kitzman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbtp/image/image.html  
Insert length: 427 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 293.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:1077066"  
/clone\_lib="NCI\_CGAP\_Pt4.1"  
/sex="male"  
/tissue\_type="prostatic intraepithelial neoplasia - high grade"  
/lab\_host="DH10B"

/note="Organ: prostate; Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center"

BASE COUNT 52 a 93 c 98 g 73 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 316;  
Best Local Similarity 100.0%; Pred. No. 0.89;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 181 GTTCTGTGACACCCAGTGGTCTC 207

RESULT 2  
AA506459 336 bp. mRNA linear. EST 20-AUG-1997  
LOCUS nh46a08.s1 NCI\_CGAP\_Pt5 Homo sapiens cDNA clone IMAGE:955382  
DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);  
ACCESSION AA506459  
VERSION AA506459  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuangui,  
M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 442 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham.

FEATURES  
source  
1..336

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:955382"  
/clone\_lib="NCI\_CGAP\_Pt5"  
/sex="male"  
/tissue\_type="prostate"  
/lab\_host="DH10B"  
/note="Vector: pAMP10; mRNA made from normal prostatic

## FEATURES

source

1..336

Location/Qualifiers

1..336

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_image="IMAGE:955382"

/clone\_lib="NCI\_CGAP\_Pt5"

/sex="male"

/tissue\_type="prostate"

/lab\_host="DH10B"

/note="Vector: pAMP10; mRNA made from normal prostatic

Epithelial cells, cDNA made by oligo-dT priming. Size-selected on agarose gel, average insert size 600 bp.

Non-directionally cloned bp.

Size-selected on agarose gel,

average insert size 600 bp.

Non-directionally cloned bp.

Size-selected on agarose gel,

average insert size 600 bp.

Epithelial cells, cDNA made by oligo-dT priming  
Non-directionally cloned. Size-selected on agarose gel,  
average insert size 600 bp.

## BASE COUNT

57 a 106 c 99 g 74 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 336;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 189 GTTCTGTGACACCCAGTGGTCTC 215

RESULT 3  
AA503943 371 bp. mRNA linear. EST 20-AUG-1997  
LOCUS nh38d05.s1 NCI\_CGAP\_Pt5 Homo sapiens cDNA clone IMAGE:954633  
DEFINITION similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);  
ACCESSION AA503943  
VERSION AA503943  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuangui,  
M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bdrrp/image/image.html  
Insert Length: 454 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 365.

FEATURES  
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1..371

/organism="Homo sapiens"  
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/clone\_image="IMAGE:954633"  
/clone\_lib="NCI\_CGAP\_Pt5"  
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/tissue\_type="prostate"  
/lab\_host="DH10B"  
/note="Vector: pAMP10; mRNA made from normal prostatic  
epithelial cells, cDNA made by oligo-dT priming. Size-selected on agarose gel,  
average insert size 600 bp.

## BASE COUNT

63 a 112 c 111 g 85 t

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 371;  
Best Local Similarity 100.0%; Pred. No. 0.9;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 182 GTTCTGTGACACCCAGTGGTCTC 208

RESULT 4  
AA603297/c



LOCUS AA603297 377 bp mRNA linear EST 21-OCT-1997  
 DEFINITION npl2c11.s1 NCI CGAP Pr3 Homo sapiens cDNA clone IMAGE:116116  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,  
 mRNA sequence.  
 ACCESSION AA603297  
 VERSION AA603297.1 GI:2437158  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 377)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,  
 Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html).  
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 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 345.  
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 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10,  
 000 microdissected cells histologically-determined to be  
 fully malignant prostate cancer cells. Double-stranded  
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR  
 applied to the cDNA with an adaptor-specific primer, and  
 the resulting PCR product subcloned into PAMP10 by the  
 UDG-cloning method (Life Technologies). Average insert  
 size is 600 bp. NOTE: Not directionally cloned. This  
 library was constructed by David Kitzman."  
 BASE COUNT 90 a 130 c 97 g 60 t  
 ORIGIN  
 Query Match 100.0%; Score 27; DB 9; Length 377;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GTTCTGTCACACCCAGTGGTCTC 27  
 |||||||||||||||||||||||||  
 Db 288 GTTCTGTCACACCCAGTGGTCTC 262  
 RESULT 5  
 LOCUS AA573604 397 bp mRNA linear EST 12-SEP-1997  
 DEFINITION n142d12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:916439  
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 mRNA sequence.  
 ACCESSION AA573604  
 VERSION AA573604.1 GI:2348132  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 397)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,  
 Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html).  
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 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 350.  
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 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMP10; Site\_1: NotI; Site\_2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10,  
 000 microdissected preneoplastic cells  
 histologically-determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 cDNA with an adaptor-specific primer, and the resulting  
 PCR product subcloned into PAMP10 by the UDG-cloning  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Kitzman."  
 BASE COUNT 78 a 124 c 116 g 79 t  
 ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 0.9;  
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 Oy 1 GTTCTGTCACACCCAGTGGTCTC 27  
 |||||||||||||||||||||||||  
 Db 95 GTTCTGTCACACCCAGTGGTCTC 121  
 RESULT 6  
 LOCUS AA177005 435 bp mRNA linear EST 14-AUG-1997  
 DEFINITION nc03b02.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:302 similar  
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 mRNA sequence.  
 ACCESSION AA177005  
 VERSION AA177005.1 GI:1758143  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 435)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.

Michael Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 DNA Sequencing by: Genome Systems Inc., Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bdip/image/image.html  
 Seq primer: -40M13 fwd. from Amersham.

## FEATURES

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 Location/Qualifiers  
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/organism="Homo sapiens"  
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 /clone\_image="302"  
 /clone\_lib="NCI-CGAP\_Pr2"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMP10; Site-1: NotI; Site-2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10  
 ,000 microdissected preneoplastic cells  
 histologically-determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 cDNA with an adaptor-specific primer, and the resulting  
 PCR product subcloned into PAMP10 by the upe-cloning  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Kitzman."

## BASE COUNT

64 a 119 c 146 g 105 t 1 others

## ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 155 GTTCTGTGACACCCAGTGGTCTC 181

## RESULT 7

AA533652 453 bp mRNA linear EST 21-AUG-1997  
 n72908.s1 NCI-CGAP\_Pr10 Homo sapiens cDNA clone IMAGE:998078  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);

## DEFINITION

mRNA sequence.  
 AA533652  
 AA533652.1 GI:2277668

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Human sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 453)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuagui,  
 M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: David B. Kitzman, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bdip/image/image.html

Trace considered overall poor quality  
 Insert Length: 1654 Std Error: 0.00  
 Seq primer: -40M13 fwd. ET from Amersham

FEATURES  
 source  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1. 435

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="998078"  
 /clone\_lib="NCI-CGAP\_Pr10"  
 /sex="male"  
 /tissue\_type="invasive prostate tumor"  
 /lab\_host="DH10B"  
 /note="Organ: prostate; Vector: PAMP10; mRNA made from  
 invasive prostate tumor. cDNA made by oligo-dT priming.  
 Non-directionally cloned. Size-selected on agarose gel,  
 average insert size 600 bp. Library made by D. Kitzman,  
 NIH."

## BASE COUNT

83 a 127 c 133 g 110 t

## ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 435;  
 Best Local Similarity 100.0%; Pred. No. 0.9; Mismatches 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTCTGTGACACCCAGTGGTCTC 27

Db 143 GTTCTGTGACACCCAGTGGTCTC 169

## RESULT 8

AI685510 454 bp mRNA linear EST 27-MAY-1999  
 tu36p10.x1 NCI-CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:2253115.3'  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);

## DEFINITION

mRNA sequence.  
 AI685510  
 AI685510.1 GI:4896804

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Human sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 454)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bdip/image/image.html  
 Seq primer: -40UP from Gibco.

## FEATURES

## source

1. 454

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="2253115"  
 /clone\_lib="NCI-CGAP\_Pr28"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

/note="Organ: prostate; Vector: pT7n3D-Pac (pharmacia)  
 with a modified polylinker; plasmid DNA from the  
 normalized library NCI-CGAP\_Pr22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clonoids  
 955608-986759, 1101192-1101959, and 1217928-1220615)."

BASE COUNT 99 a 137 c 109 g 109 t  
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 454;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
 Db 356 GTTCTGTCACCCCGAGTGGTCCTC 330

RESULT 9  
 LOCUS BI046475 465 bp mRNA linear EST 14-JUN-2001  
 DEFINITION NR3-FN0209-070201-010-b11 FN0209 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BI046475  
 VERSION BI046475.1 GI:14453097  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 465)  
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,E.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?PL=NR3&t2=NR3-FN0209-  
 070201-010-b11&t3=2001-02-07&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 7  
 location/Qualifiers  
 1.465  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FN0209"  
 /dev\_stage="Adult"  
 /note="Organ: prostate,normal; Vector: puc18; Site\_1: SmaI  
 ; Site\_2: SmaI; A mini-library was made by cloning  
 products derived from ORESTES PCR (U.S. Letters Patent  
 application No. 196,716 - Ludwig Institute for Cancer  
 Research) profiles into the pUC 18 vector. Reverse  
 transcription of tissue mRNA and cDNA amplification were  
 performed under low stringency conditions."

BASE COUNT 83 a 134 c 144 g 103 t  
 ORIGIN 1 others

Query Match 100.0%; Score 27; DB 13; Length 465;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
 Db 323 GTTCTGTCACCCCGAGTGGTCCTC 349

RESULT 10  
 LOCUS AI525128 470 bp mRNA linear EST 09-AUG-1999

DEFINITION Promena-7.F01.r bvtumor Homo sapiens cDNA 5', mRNA sequence.  
 ACCESSION AI525128  
 VERSION AI525128.1 GI:14439263  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 470)  
 Huang,G.M., Ng,W.I., Parkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.  
 and Hood,L.  
 Prostate cancer expression profiling by cDNA sequencing analysis  
 Genomics 59 (2), 178-186 (1999)  
 99339982  
 COMMENT Contact: Guyang Matthew Huang  
 Leroy Hood  
 University of Washington  
 Department of Molecular Biotechnology, Box 357730, University of  
 Washington, Seattle, WA 98195  
 Tel: 5106280100  
 Fax: 5106280108  
 Email: huangm@yahoo.com.

FEATURES  
 source 1.470  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="bvtumor"  
 /note="Organ: Prostate; Vector: pBluescript; Directional  
 cDNA library was constructed using Lambda ZP II kit  
 (Stratagene). mRNA was extracted from a fresh prostate  
 tumor tissues (Urology Department, University of  
 Washington)."

BASE COUNT 87 a 104 c 126 g 118 t 35 others  
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 0.9;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
 Db 186 GTTCTGTCACCCCGAGTGGTCCTC 212

RESULT 11  
 LOCUS AA603529 484 bp mRNA linear EST 08-OCT-1997  
 DEFINITION np1508.s1 NCI-CGAP-P3 Homo sapiens cDNA clone IMAGE:1116375  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);,  
 mRNA sequence.

ACCESSION AA603529  
 VERSION AA603529.1 GI:2437390  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 484)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.,  
 Michael Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Kitzman, Ph.D.  
 cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
[www.bio.linn.gov/bdrip/image/image.html](http://www.bio.linn.gov/bdrip/image/image.html)

Insert Length: 902 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 325.  
 Location/Qualifiers

## FEATURES

Source

1. 484  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:116375"  
 /clone\_lib="NCI-CGAP\_P3"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI0; Site.1: NotI; Site.2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10  
 /000 microdissected cells histologically-determined to be  
 /000 malignant prostate cancer cells. Double-stranded  
 cDNA was ligated to EcoRI adaptors, 5 cycles of PCR  
 applied to the cDNA with an adaptor-specific primer, and  
 the resulting PCR product subcloned into PAMPI0 by the  
 unc-priming method (Life Technologies). Average insert  
 size is 600 bp. NOTE: Not directionally cloned. This  
 library was constructed by David Krizman."  
 BASE COUNT 89 a 151 c 140 g 104 t  
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 0.91;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGTCACCCAGTGGTCTC 27  
 Db 187 GTTCTGTGTCACCCAGTGGTCTC 213

## RESULT 12

AA573575

## LOCUS

AA573575 485 bp mRNA linear EST 12-SEP-1997  
 n1a1f10.s1 NCI-CGAP\_P2 Homo sapiens cDNA clone IMAGE:916363  
 similar to gb:M21895 PROSTATE SPECIFIC ANTIGEN PROCURSOR (HUMAN);

## ACCESSION

AA573575

## VERSION

AA573575.1

## KEYWORDS

EST

## SOURCE

human

## ORGANISM

human

## REFERENCE

1 (bases 1 to 485)

## AUTHORS

NCI-CGAP

## TITLE

NCI-CGAP

## JOURNAL

NCI-CGAP

## COMMENT

NCI-CGAP

## FEATURES

Source

Trace considered overall poor quality  
 Insert Length: 1535 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

## source

1. 485  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:916363"  
 /clone\_lib="NCI-CGAP\_P2"  
 /sex="Male"  
 /dev\_stage="45 years old"  
 /lab\_host="DH10B"  
 /note="Vector: PAMPI0; Site.1: NotI; Site.2: EcoRI; 1st  
 strand cDNA was primed with oligo(dT)17 on 50 ng of  
 DNase-treated, total cellular RNA obtained from 5,000-10  
 /000 microdissected preneoplastic cells. Double-stranded  
 histologically-determined to be prostatic intraepithelial  
 neoplasia 2 (PIN2) cells. Double-stranded cDNA was  
 ligated to EcoRI adaptors, 5 cycles of PCR applied to the  
 cDNA with an adaptor-specific primer, and the resulting  
 PCR product subcloned into PAMPI0 by the unc-priming  
 method (Life Technologies). Average insert size is 600  
 bp. NOTE: Not directionally cloned. This library was  
 constructed by David Krizman."  
 BASE COUNT 97 a 144 c 142 g 102 t  
 ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 0.91;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTGTGTCACCCAGTGGTCTC 27  
 Db 85 GTTCTGTGTCACCCAGTGGTCTC 111

## RESULT 13

BB840533

## LOCUS

BB840533 495 bp mRNA linear EST 22-SEP-2000  
 RCI-FN0188-260700-022-f06 FN0188 Homo sapiens cDNA, mRNA sequence.

## ACCESSION

BB840533

## VERSION

BB840533.1

## KEYWORDS

EST

## SOURCE

human

## ORGANISM

human

## REFERENCE

1 (bases 1 to 495)

## AUTHORS

NCI-CGAP

## TITLE

NCI-CGAP

## JOURNAL

NCI-CGAP

## COMMENT

NCI-CGAP

Trace considered overall poor quality  
 Insert Length: 1535 Std Error: 0.00  
 Seq primer: puc 18 forward  
 High quality sequence stop: 495.  
 Location/Qualifiers

## FEATURES

Source

1. 495  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FN0188"

```

/dev_stage="Adult"
/note="Organ: prostate,normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      125 a      161 c      131 g      77 t      1 others
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTTCTGGTGCACCCCACTGGTCTC 27
Db      307 GTTCTGGTGCACCCCACTGGTCTC 281

RESULT 14
BE840441/c      505 bp      mRNA      linear      EST 22-SEP-2000
LOCUS      BE840441
DEFINITION      R01-FN0188-210700-021-a02 FN0188 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BE840441
VERSION      BE840441.1 GI:10272819
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 505)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=RC1-FN0188-210
700-021-a02&t3=2000-07-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 505.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="FN0188"
/dev_stage="Adult"
/note="Organ: prostate,normal; Vector: puc18; Site_1: SmaI
; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
Application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
BASE COUNT      127 a      164 c      136 g      78 t
ORIGIN
Query Match      100.0%; Score 27; DB 12; Length 505;

```

```

Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTTCTGGTGCACCCCACTGGTCTC 27
Db      304 GTTCTGGTGCACCCCACTGGTCTC 278

RESULT 15
AA639901      523 bp      mRNA      linear      EST 23-OCT-1997
LOCUS      AA639901
DEFINITION      np08103.s1 NCI-CGAP_P3 Homo sapiens cDNA clone IMAGE:1115741
similar to gb:M1895 PROSTATE SPECIFIC ANTIGEN PRECURSOR (HUMAN);.
mRNA sequence.
ACCESSION      AA639901
VERSION      AA639901.1 GI:2563680
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 523)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@emall.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuagui, M.D.
, Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linn.gov/bdrr/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 367.
Location/Qualifiers
1..523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="IMAGE:1115741"
/clone_1lb="NCI-CGAP_P3"
/sex="Male"
/dev_stage="45 years old"
/lab_host="DH10B"
/note="Vector: pAMP10; Site_1: NciI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected cells histologically-determined to be
fully malignant prostate cancer cells. Double-stranded
cDNA was ligated to EcoRI adaptors, 5 cycles of PCR
applied to the cDNA with an adaptor-specific primer, and
the resulting PCR product subcloned into pAMP10 by the
UDC-cloning method (Life Technologies). Average insert
size is 600 bp. NOTE: Not directionally cloned. This
library was constructed by David Krizman."
BASE COUNT      100 a      160 c      152 g      111 t
ORIGIN
Query Match      100.0%; Score 27; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GTTCTGGTGCACCCCACTGGTCTC 27
Db      187 GTTCTGGTGCACCCCACTGGTCTC 213

Search completed: November 19, 2002, 05:17:31
Job time : 1545.46 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 52.9615 seconds

: (without alignments)  
156.345 Million cell updates/sec

Title: US-09-829-004a-8

Perfect score: 27

Sequence: 1 gtctctgtgaccaccagtggtctc 27

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

## Database :

Issued Patents-NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/5B\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	200	1	US-08-931-981A-1
2	27	100.0	711	4	US-09-100-264-4
3	27	100.0	992	1	US-08-358-782D-13
4	27	100.0	992	2	US-08-764-527A-13
5	27	100.0	1350	4	US-09-605-785-616
6	27	100.0	1462	1	US-08-358-782D-14
7	27	100.0	1462	1	US-08-764-527A-14
8	27	100.0	1729	2	US-08-844-024-1
9	27	100.0	1729	2	US-08-718-547-1
10	27	100.0	7130	4	US-09-056-105-31
11	23.8	88.1	711	3	US-08-622-046B-2
12	23.8	88.1	711	3	US-08-622-046B-13
13	23.8	88.1	711	4	US-09-100-264-2
14	23.8	88.1	760	3	US-08-768-859A-7
15	23.8	88.1	760	3	US-08-767-820A-7
16	23.8	88.1	760	5	PCT-US95-06157-7
17	23.8	88.1	766	3	US-08-768-859A-9
18	23.8	88.1	766	3	US-08-767-820A-9
19	23.8	88.1	766	3	US-08-622-046B-6
20	23.8	88.1	766	3	US-08-622-046B-17
21	23.8	88.1	766	4	US-09-100-264-6
22	23.8	88.1	766	4	PCT-US95-06157-9
23	23.8	88.1	822	4	US-09-100-264-8
24	23.8	88.1	832	3	US-08-768-859A-5
25	23.8	88.1	832	3	US-08-768-859A-20
26	23.8	88.1	832	3	US-08-767-820A-5
27	23.8	88.1	832	3	US-08-767-820A-20

28	23.8	88.1	832	3	US-08-622-046B-4	Sequence 4, Appl
29	23.8	88.1	832	5	US-08-622-046B-15	Sequence 15, Appl
30	23.8	88.1	832	5	PCT-US95-06157-5	Sequence 5, Appl
31	23.8	88.1	1341	4	US-08-983-075D-6	Sequence 6, Appl
32	23.8	88.1	1358	4	US-08-983-075D-8	Sequence 8, Appl
33	21	77.8	21	4	US-09-493-491-11	Sequence 11, Appl
34	21	77.8	21	4	US-09-493-491-24	Sequence 24, Appl
35	20.6	76.3	1364	4	US-09-280-116-20	Sequence 20, Appl
36	19.6	72.6	45	4	US-09-605-785-790	Sequence 790, App
37	19.6	72.6	216	4	US-09-280-116-6	Sequence 6, Appl
38	19.6	72.6	234	4	US-09-605-785-328	Sequence 328, App
39	19.6	72.6	234	4	US-09-439-313-328	Sequence 328, App
40	19.6	72.6	234	4	US-09-352-616A-328	Sequence 328, App
41	19.6	72.6	234	4	US-09-232-149A-328	Sequence 328, App
42	19.6	72.6	700	4	US-09-280-116-68	Sequence 68, Appl
43	19.6	72.6	765	4	US-09-605-785-524	Sequence 524, App
44	19.6	72.6	765	4	US-09-439-313-524	Sequence 524, App
45	19.6	72.6	871	1	US-08-744-026-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-931-981A-1  
Sequence 1, Application US/08931981A  
Patent No. 5817798  
GENERAL INFORMATION:  
APPLICANT: G. Gundling  
TITLE OF INVENTION: RAPID RNA ISOLATION PROCEDURE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,981A  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul D. Yasger  
REGISTRATION NUMBER: 37,477  
REFERENCE/DOCKET NUMBER: 6179.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/938-3508  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ. ID NO.: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA (PSA exons 2 and 3)  
US-08-931-981A-1

Query Match 100.0%; Score 27; DB 1; Length 200;  
Best Local Similarity 100.0%; Pred. No. 0.0062;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCAAGTGGTCCTC 27  
DB 120 GTTCTGTGACCCCAAGTGGTCCTC 146

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RESULT 2
US-09-100-264-4
; Sequence 4, Application US/09100264
; Patent No. 6235486
; GENERAL INFORMATION:
; APPLICANT: Young, Charles Y.F.
; APPLICANT: Tindall, Donald J.
; TITLE OF INVENTION: Method for detection of breast cancer
; FILE REFERENCE: 545.006U51
; CURRENT APPLICATION NUMBER: US/09/100.264
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 60/050.963
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-100-264-4

Query Match
Best Local Similarity 100.0%; Score 27; DB 4; Length 711;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGTCACCCCGAGTGCTCTC 27
Db 85 GTTCTGTGTCACCCCGAGTGCTCTC 111

RESULT 3
US-08-358-782D-13
; Sequence 13, Application US/08358782D
; Patent No. 5674682
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358.782D
; FILING DATE: 15-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: TJU-1327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; ANTI-SENSE: NO
US-08-358-782D-13

Query Match
Best Local Similarity 100.0%; Score 27; DB 1; Length 992;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGTCACCCCGAGTGCTCTC 27
Db 200 GTTCTGTGTCACCCCGAGTGCTCTC 226

RESULT 4
US-08-764-527A-13
; Sequence 13, Application US/08764527A
; Patent No. 5939258
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764.527A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358.782
; FILING DATE: 15-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: TJU-1327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 992 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-764-527A-13

Query Match
Best Local Similarity 100.0%; Score 27; DB 2; Length 992;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGTCACCCCGAGTGCTCTC 27
Db 200 GTTCTGTGTCACCCCGAGTGCTCTC 226

RESULT 5
US-09-605-785-616
; Sequence 616, Application US/09605785
```



Patent No. 6321716  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqun  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C16  
CURRENT APPLICATION NUMBER: US/09/605,785  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 1350  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-605-785-616

Query Match 100.0%; Score 27; DB 4; Length 1350;  
Best Local Similarity 100.0%; Pred. No. 0.0072;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
|||||  
Db 778 GTTCTGTCACCCCGAGTGGTCCTC 804

RESULT 6  
US-08-358-782D-14  
Sequence 14, Application US/08358782D  
Patent No. 5674682  
GENERAL INFORMATION:  
APPLICANT: Cioce, Carlo  
APPLICANT: Gomella, Leonard  
APPLICANT: Mulholland, S. Grant  
APPLICANT: Moreno, Jose  
APPLICANT: Fischer, Rainer  
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th. Floor  
City: Philadelphia  
STATE: PA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782D  
FILING DATE: 15-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-358-782D-14

Query Match 100.0%; Score 27; DB 1; Length 1462;  
Best Local Similarity 100.0%; Pred. No.: 0.0073;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTCTGTCACCCCGAGTGGTCCTC 27  
|||||  
Db 181 GTTCTGTCACCCCGAGTGGTCCTC 207

RESULT 7  
US-08-764-527A-14  
Sequence 14, Application US/08764527A  
Patent No. 5938258  
GENERAL INFORMATION:  
APPLICANT: Cioce, Carlo  
APPLICANT: Gomella, Leonard  
APPLICANT: Mulholland, S. Grant  
APPLICANT: Moreno, Jose  
APPLICANT: Fischer, Rainer  
TITLE OF INVENTION: Methods of Detecting Micrometastasis of  
TITLE OF INVENTION: Prostate  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th. Floor  
City: Philadelphia  
STATE: PA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,527A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782  
FILING DATE: 15-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-764-527A-14

Query Match 100.0%; Score 27; DB 2; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 0.0073;

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Page 4

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACACCCCACTGGTCTC 27  
|||||  
Db 181 GTTCTGTCACACCCCACTGGTCTC 207

RESULT 8  
US-08-844-024-1  
; Sequence 1, Application US/08844024  
; Patent No. 5840494  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Aaron E., et al.  
; TITLE OF INVENTION: A Method For Molecular Staging Of  
; TITLE OF INVENTION: Prostate Cancer  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/844,024  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/229,391  
; FILING DATE: 15-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 43677/JPM/TEP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1729 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 378..1088  
US-08-844-024-1

Query Match 100.0%; Score 27; DB 2; Length 1729;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACACCCCACTGGTCTC 27  
|||||  
Db 462 GTTCTGTCACACCCCACTGGTCTC 488

RESULT 9  
US-08-718-547-1  
; Sequence 1, Application US/08718547  
; Patent No. 5976794  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Aaron E.; Butyan, Ralph; Rafo, Anthony;  
; APPLICANT: Olsson, Carl A.

; TITLE OF INVENTION: A Method For Molecular Staging Of  
; TITLE OF INVENTION: Prostate Cancer  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,547  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 43677-A-PCT/JPM/MUG  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1729 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 378..1088  
US-08-718-547-1

Query Match 100.0%; Score 27; DB 2; Length 1729;  
Best Local Similarity 100.0%; Pred. No. 0.0074;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTCACACCCCACTGGTCTC 27  
|||||  
Db 462 GTTCTGTCACACCCCACTGGTCTC 488

RESULT 10  
US-09-056-105-31  
; Sequence 31, Application US/09056105  
; Patent No. 6287569  
; GENERAL INFORMATION:  
; APPLICANT: KIPPS, THOMAS J.  
; APPLICANT: WU, YUNQI  
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
; TITLE OF INVENTION: PROCESSING  
; FILE REFERENCE: 233/221  
; CURRENT APPLICATION NUMBER: US/09/056,105  
; CURRENT FILING DATE: 1998-04-06  
; EARLIER APPLICATION NUMBER: 60/043,467  
; EARLIER FILING DATE: 1997-04-10  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 7130  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-056-105-31

Query Match 100.0%; Score 27; DB 4; Length 7130;

Best Local Similarity 100.0%; Pred. No. 0.0082;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
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Db 2069 GTTCTGTGACCCCGAGTGGTCTC 2095

## RESULT 11

US-08-622-046B-2  
; Sequence 2, Application US/08622046B  
; Patent No. 6103237  
; GENERAL INFORMATION:  
; APPLICANT: Saedi, Mohammed S.  
; TITLE OF INVENTION: Stable Variant HK2 Polypeptide  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.  
; STREET: P.O. Box 2938  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 26-MARCH-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Woessner, Warren D.  
; REGISTRATION NUMBER: 30,440  
; REFERENCE/DOCKET NUMBER: 476.001US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-373-6903  
; TELEFAX: 612-339-3061  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 711 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-622-046B-2

Query Match 88.1%; Score 23.8; DB 3; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
|||  
Db 85 GTCTGTGACCCCGAGTGGTCTC 111

## RESULT 12

US-08-622-046B-13  
; Sequence 13, Application US/08622046B  
; Patent No. 6103237  
; GENERAL INFORMATION:  
; APPLICANT: Saedi, Mohammed S.  
; APPLICANT: Mikolajczyk, Stephen D.  
; TITLE OF INVENTION: Stable Variant HK2 Polypeptide  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.  
; STREET: P.O. Box 2938  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/622,046B

FILING DATE: 26-MARCH-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 476.001US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-373-6903

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 711 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-622-046B-13

Query Match 88.1%; Score 23.8; DB 3; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
|||  
Db 85 GTCTGTGACCCCGAGTGGTCTC 111

## RESULT 13

US-09-100-264-2  
; Sequence 2, Application US/09100264  
; Patent No. 6235486  
; GENERAL INFORMATION:  
; APPLICANT: Young, Charles Y.F.  
; APPLICANT: Tindall, Donald J.  
; APPLICANT: Klee, George G.  
; TITLE OF INVENTION: Method for detection of breast cancer  
; FILE REFERENCE: 545.006US1  
; CURRENT APPLICATION NUMBER: US/09/100,264  
; CURRENT FILING DATE: 1998-06-19  
; EARLIER APPLICATION NUMBER: US 60/050,963  
; EARLIER FILING DATE: 1997-06-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 2  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-100-264-2

Query Match 88.1%; Score 23.8; DB 4; Length 711;

Best Local Similarity 92.6%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCTGTGACCCCGAGTGGTCTC 27  
|||  
Db 85 GTCTGTGACCCCGAGTGGTCTC 111

## RESULT 14

US-08-768-859A-7  
; Sequence 7, Application US/08768859A  
; Patent No. 6013471  
; GENERAL INFORMATION:  
; APPLICANT: Tindall, Donald J.  
; APPLICANT: Young, Charles Y.F.

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Page 6

APPLICANT: Saedi, Mohammed S.  
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/768,859A  
FILING DATE: 17-DECEMBER-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 545.002US3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 760 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 7..720  
US-08-768-859A-7

Query Match 88.1%; Score 23.8; DB 3; Length 760;  
Best Local Similarity 92.6%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27  
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DB 94 GTTCGTGTCACCCCGAGTGGTCTC 120

RESULT 15  
US-08-767-820A-7  
Sequence 7, Application US/08767820A  
Patent No. 6093796  
GENERAL INFORMATION:  
APPLICANT: Tindall, Donald J.  
APPLICANT: Young, Charles Y.F.  
APPLICANT: Saedi, Mohammed S.  
TITLE OF INVENTION: DNA Encoding HK2 Variant Polypeptides  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/767,820A  
FILING DATE: 17-DECEMBER-1996  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.  
REGISTRATION NUMBER: 30,440  
REFERENCE/DOCKET NUMBER: 545.002US2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 760 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 7..720  
US-08-767-820A-7

Query Match 88.1%; Score 23.8; DB 3; Length 760;  
Best Local Similarity 92.6%; Pred. No. 0.15;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27  
|||  
DB 94 GTTCGTGTCACCCCGAGTGGTCTC 120

Search completed: November 19, 2002, 05:20:21  
Job time : 53.9615 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 04:04:51 ; Search time 91.3846 Seconds  
(without alignments)  
111.898 Million cell updates/sec

Title: US-09-829-004A-8

Perfect score: 27  
Sequence: 1 gttctgtgtcaccacccagtggtcttc 27

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

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3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
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7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	27	100.0	27	10	US-09-829-004A-8
2	27	100.0	1350	10	US-09-759-143-616
3	27	100.0	1350	10	US-09-780-669-616
4	27	100.0	1350	10	US-09-822-827-616
5	27	100.0	1759	10	US-09-969-708-598
6	27	100.0	1758	10	US-09-822-827-977
7	27	100.0	2406	10	US-09-822-827-980
8	27	100.0	3423	10	US-09-755-100-5
9	27	100.0	3846	10	US-09-755-100-3
10	27	100.0	4661	10	US-09-755-100-1
11	27	100.0	4661	10	US-09-755-100-2
12	27	100.0	1678	10	US-09-925-300-153
13	27	100.0	861	10	US-09-925-297-286
14	27	100.0	871	10	US-09-962-833-101
15	27	100.0	871	10	US-09-880-107-2307
16	27	100.0	316	10	US-09-925-300-814
17	27	100.0	45	10	US-09-759-143-790
18	27	100.0	45	10	US-09-780-669-790
19	27	100.0	45	10	US-09-822-827-790

20	19.6	72.6	234	10	US-09-759-143-328	Sequence 328, App
21	19.6	72.6	234	10	US-09-780-669-328	Sequence 328, App
22	19.6	72.6	234	10	US-09-822-827-328	Sequence 328, App
23	19.6	72.6	765	10	US-09-759-143-524	Sequence 524, App
24	19.6	72.6	765	10	US-09-780-669-524	Sequence 524, App
25	19.6	72.6	765	10	US-09-822-827-524	Sequence 524, App
26	19.6	72.6	871	10	US-09-956-999-7	Sequence 7, Appl
27	19.6	72.6	1119	10	US-09-759-143-177	Sequence 177, App
28	19.6	72.6	1119	10	US-09-780-669-177	Sequence 177, App
29	19.6	72.6	1119	10	US-09-030-606-177	Sequence 177, App
30	19.6	72.6	1119	10	US-09-822-827-177	Sequence 177, App
31	19.6	72.6	1119	10	US-09-115-453-177	Sequence 175, App
32	19.6	72.6	1167	10	US-09-759-143-175	Sequence 175, App
33	19.6	72.6	1167	10	US-09-780-669-175	Sequence 175, App
34	19.6	72.6	1167	10	US-09-030-606-175	Sequence 175, App
35	19.6	72.6	1167	10	US-09-822-827-175	Sequence 175, App
36	19.6	72.6	1167	10	US-09-115-453-175	Sequence 175, App
37	19.6	72.6	1214	10	US-09-759-143-225	Sequence 225, App
38	19.6	72.6	1214	10	US-09-780-669-225	Sequence 225, App
39	19.6	72.6	1214	10	US-09-822-827-225	Sequence 225, App
40	19.6	72.6	1214	10	US-09-115-453-225	Sequence 225, App
41	19.6	72.6	1215	10	US-09-759-143-326	Sequence 326, App
42	19.6	72.6	1215	10	US-09-780-669-326	Sequence 326, App
43	19.6	72.6	1215	10	US-09-822-827-326	Sequence 326, App
44	19.6	72.6	1248	10	US-09-759-143-171	Sequence 171, App
45	19.6	72.6	1248	10	US-09-780-669-171	Sequence 171, App

## ALIGNMENTS

RESULT 1  
US-09-829-004A-8  
; Sequence 8, Application US/09829004A  
; Patent No. US20020132976A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific Antigen (P  
; FILE REFERENCE: 11014-24  
; CURRENT APPLICATION NUMBER: US/09/829,004A  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 60/195,456  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CLP314  
US-09-829-004A-8  
Query Match 100.0%; Score 27; DB 10; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTTCTGTGACCCCGAGTGAGTCTC 27  
DB 1 GTTCTGTGACCCCGAGTGAGTCTC 27  
RESULT 2  
US-09-759-143-616  
; Sequence 616, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.

```

: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolck, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C23
: CURRENT APPLICATION NUMBER: US/09/759,143
: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-759-143-616

Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
DB 778 GTTCTGTGCACCCCGAGTGGTCTC 804

RESULT 3
: Sequence 616, Application US/09780669
: Patent No. US20020051977A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolck, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780,669
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-780-669-616
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Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
DB 778 GTTCTGTGCACCCCGAGTGGTCTC 804

RESULT 4
: Sequence 616, Application US/09822827
: Patent No. US20020081680A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822,827
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 616
: LENGTH: 1350
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-822-827-616

Query Match      100.0%; Score 27; DB 10; Length 1350;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
DB 778 GTTCTGTGCACCCCGAGTGGTCTC 804

RESULT 5
: Sequence 398, Application US/09969708
: Patent No. US20020102532A1
: GENERAL INFORMATION:
: APPLICANT: Augustus, Meena
: TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
: FILE REFERENCE: 689290-70
: CURRENT APPLICATION NUMBER: US/09/969,708
: CURRENT FILING DATE: 2001-10-03
: PRIOR APPLICATION NUMBER: US/60/237,606
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,608
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: US/60/237,425
: PRIOR FILING DATE: 2000-10-03
: NUMBER OF SEQ ID NOS: 658
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 598
: LENGTH: 1729
: TYPE: DNA
: ORGANISM: Homosapiens
: US-09-969-708-598

Query Match      100.0%; Score 27; DB 10; Length 1729;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTGTGCACCCCGAGTGGTCTC 27
DB 462 GTTCTGTGCACCCCGAGTGGTCTC 488

RESULT 6
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US-09-822-827-977
; Sequence 977, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 977
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-977

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 1758;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCTGTGCACCCCACTGGGTCTC 27
Db 1186 GTCTGTGCACCCCACTGGGTCTC 1212

RESULT 7
US-09-822-827-980
; Sequence 980, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 980
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-980

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 2406;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCTGTGCACCCCACTGGGTCTC 27
Db 778 GTCTGTGCACCCCACTGGGTCTC 804

RESULT 8
US-09-755-100-5
; Sequence 5, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5
; LENGTH: 3423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-5

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 3423;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCTGTGCACCCCACTGGGTCTC 27
Db 1658 GTCTGTGCACCCCACTGGGTCTC 1684

RESULT 9
US-09-755-100-3
; Sequence 3, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3846
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-3

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 3846;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCTGTGCACCCCACTGGGTCTC 27
Db 2081 GTCTGTGCACCCCACTGGGTCTC 2107

RESULT 10
US-09-755-100-1
; Sequence 1, Application US/09755100
; Patent No. US20020099189A1
; GENERAL INFORMATION:
; APPLICANT: SAVITZKY, Kinneret et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES
; FILE REFERENCE: 2786-0156P
; CURRENT APPLICATION NUMBER: US/09/755,100
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: IL 128587
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: IL 129439
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: IL 131363
; PRIOR FILING DATE: 1999-08-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-755-100-1

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 4661;
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Best Local Similarity 100.0%; Pred. No. 0.0096;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27  
Db 2896 GTTCGTGTCACCCCGAGTGGTCTC 2922

RESULT 11  
US-09-755-100-2

; Sequence 2, Application US/09755100  
; Patent No. US2002009189A1  
; GENERAL INFORMATION:  
; APPLICANT: SAVITZKY, Kinmeret et al.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES  
; FILE REFERENCE: 2/86-0156P  
; CURRENT APPLICATION NUMBER: US/09/755,100  
; PRIOR FILING DATE: 2001-01-08  
; PRIOR APPLICATION NUMBER: IL 128587  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: IL 129439  
; PRIOR FILING DATE: 1999-04-14  
; PRIOR APPLICATION NUMBER: IL 131363  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO: 2  
; LENGTH: 4661  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-755-100-2

Query Match  
Best Local Similarity 100.0%; Score 27; DB 10; Length 4661;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27  
Db 2896 GTTCGTGTCACCCCGAGTGGTCTC 2922

RESULT 12  
US-09-925-300-153

; Sequence 153, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen,  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO: 153  
; LENGTH: 1678  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1663)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-153

Query Match  
Best Local Similarity 92.6%; Score 23.8; DB 10; Length 1678;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTCGTGTCACCCCGAGTGGTCTC 27

Db 345 GTTCGTGTCACCCCGAGTGGTCTC 371

RESULT 13  
US-09-925-297-286

; Sequence 286, Application US/09925297  
; Patent No. US20020081659A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: P105  
; CURRENT APPLICATION NUMBER: US/09/925,297  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05989  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; NUMBER OF SEQ ID NOS: 928  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO: 286  
; LENGTH: 861  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-297-286

Query Match  
Best Local Similarity 78.5%; Score 21.2; DB 10; Length 861;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTGTGTCACCCCGAGTGGTCTC 27  
Db 173 TTCTGTGTCACCCCGAGTGGTCTC 198

RESULT 14  
US-09-962-832-101

; Sequence 101, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign  
; FILE REFERENCE: 689290-74  
; CURRENT APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,077  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,280  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: Patentln version 3.0  
; SEQ ID NO: 101  
; LENGTH: 871  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-962-832-101

Query Match  
Best Local Similarity 78.5%; Score 21.2; DB 10; Length 871;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTCTGTGTCACCCCGAGTGGTCTC 27  
Db 194 TTCTGTGTCACCCCGAGTGGTCTC 219

RESULT 15  
US-09-880-107-2307

; Sequence 2307, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.





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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 23:02:59 : Search time 191.769 Seconds  
(without alignments)  
317.068 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	22	AAD21363
2	27	100.0	90	18	AAT90073
3	27	100.0	246	18	AAT90074
4	27	100.0	420	23	ABV38513
5	27	100.0	429	23	ABV14332
6	27	100.0	466	23	ABV44545
7	27	100.0	476	23	ABV35419
8	27	100.0	492	23	ABV07463
9	27	100.0	616	23	ABV44248

C	10	27	100.0	632	23	ABV37397	Human prostate exp
	11	27	100.0	639	18	AAT92976	CDNA for prostate
	12	27	100.0	651	23	AAT22297	Human prostate exp
	13	27	100.0	651	23	ABV28130	Human prostate exp
	14	27	100.0	711	20	AXX08947	Human prostate spe
	15	27	100.0	744	24	ABK66205	CDNA encoding huma
	16	27	100.0	841	23	ABV25078	Human prostate exp
	17	27	100.0	990	21	AAZ47134	Human prostate-spe
	18	27	100.0	992	18	AAT91054	Human prostate spe
	19	27	100.0	992	18	AXX99846	Prostate specific
	20	27	100.0	1021	23	ABV24907	Human prostate exp
	21	27	100.0	1021	23	ABV29761	Human prostate exp
	22	27	100.0	1066	21	AAC03740	Human secreted pfp
	23	27	100.0	1329	23	ABV23473	Human prostate exp
	24	27	100.0	1329	23	ABV29201	Human prostate exp
	25	27	100.0	1350	22	AAS63953	Human cDNA encodin
	26	27	100.0	1350	22	AAH38860	Human P703P/PSA fu
	27	27	100.0	1350	24	ABL95324	Human prostate exp
	28	27	100.0	1397	23	ABV23260	Prostate specific
	29	27	100.0	1445	19	AAV32497	Human prostate spe
	30	27	100.0	1462	18	AAT91055	Human prostate spe
	31	27	100.0	1462	20	AXX99847	Prostate specific
	32	27	100.0	1466	19	AAV32496	Prostate specific
	33	27	100.0	1466	21	AAV11711	Human prostate-spe
	34	27	100.0	1728	17	AAT35867	Prostate-specific
	35	27	100.0	1729	16	AAT04864	Prostate-specific
	36	27	100.0	1729	24	ABL69732	Prostate cancer re
	37	27	100.0	1866	23	ABV23503	Human prostate exp
	38	27	100.0	1866	23	ABV23503	Human prostate exp
	39	27	100.0	1866	23	ABV24768	Human prostate exp
	40	27	100.0	1866	23	ABV29105	Human prostate exp
	41	27	100.0	1866	23	ABV29105	Human prostate exp
	42	27	100.0	1866	23	ABV29105	Human prostate exp
	43	27	100.0	1866	23	ABV29331	Human prostate exp
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	45	27	100.0	2106	22	AAF66958	Human WT1/PSA fusi

## ALIGNMENTS

RESULT 1	
AAD21363	standard; DNA: 27 BP.
AC	AAD21363;
DT	28-JAN-2002 (first entry)
XX	Prostate specific antigen (PSA) derived peptide, CLP316 encoding DNA.
XX	Prostate-specific antigen; PSA: immunogenic peptide; immune response;
KW	therapy: cancer; prostate cancer; tumour metastasis; prophylaxis; ds.
KW	therapy: cancer; prostate cancer; tumour metastasis; prophylaxis; ds.
XX	Unidentified.
OS	Unidentified.
XX	Unidentified.
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	1..27
FT	/*tag= a
FT	/product= "PSA derived peptide, CLP316"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	WO200176622-A2.
XX	18-OCT-2001.
PD	10-APR-2001; 2001WO-CA00473.
XX	10-APR-2001; 2000US-195456P.
XX	10-APR-2000; 2000US-195456P.
XX	(AVET ) AVENTIS PASTEUR LTD.
PA	(AVET ) AVENTIS PASTEUR LTD.
XX	(AVET ) AVENTIS PASTEUR LTD.

PI Pedyczak A, Chong P, Sia CDY;  
 XX WPI: 2001-663015/76.  
 DR P-PSDB: AAEL3025.  
 XX  
 XX New polypeptide, useful for treating cancers such as prostate cancer,  
 PT comprises prostate-specific antigen derived peptide -  
 XX  
 PS Claim 7: Page 28; 41pp: English.  
 XX  
 CC The patent discloses immunogenic peptides of prostate-specific antigen  
 CC (PSA) and nucleic acids encoding them. The peptides of the invention  
 CC are used to prepare a medicament to elicit an immune response in an  
 CC animal. They are used to treat cancer such as prostate cancer and  
 CC tumour metastasis. They are also useful for prophylaxis, for  
 CC preparing monoclonal or polyclonal antibodies, and in conventional  
 CC techniques of immunology, molecular biology, cell biology and  
 CC recombinant DNA technology. The present sequence is a DNA encoding  
 CC PSA derived peptide, CLP316.  
 CC  
 SQ Sequence 27 BP; 6 A; 6 G; 9 T; 0 other;  
 Query Match 100.0%; Score 27; DB 22; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.0051;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AACTTCAGTGTGTGACCTCATGTT 27  
 DB 1 AACTTCAGTGTGTGACCTCATGTT 27  
 RESULT 2  
 AAT90073 standard; cDNA; 90 BP.  
 ID AAT90073  
 AC AAT90073;  
 DT 14-APR-1998 (first entry)  
 XX  
 DE Prostate specific antigen oligo-epitope encoding DNA.  
 XX  
 KM Prostate-specific antigen; PSA; epitope; vaccine; immune response;  
 KM Prostatic tumour cell; human leukocyte antigen; HLA; cytotoxic;  
 KM T lymphocyte; cancer; ds.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT misc\_difference 58..60  
 FT /\*tag- a  
 FT /transl\_except- (pos:58..60,aa:Cys)  
 XX  
 PD WO9735021-A2.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PD 19-MAR-1997; 97WO-US04454.  
 XX  
 PD 20-MAR-1996; 96US-0618936.  
 XX  
 PA (USSH ) US SEC DEPT HEALTH.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Schlom J, Tsang K, Zaremba S;  
 XX  
 DR WPI: 1997-480226/44.  
 DR P-PSDB: AAW27387.  
 XX  
 PT Prostate specific antigen multiple epitope peptide - useful in  
 PT vaccine to produce immune response against prostate specific antigen  
 PT in prostatic tumour cell  
 XX

PS Claim 21; Page 64; 85pp: English.  
 XX  
 CC The present sequence encodes a prostate specific antigen oligo-epitope  
 CC peptide (PSA-OP) of the present invention. The PSA-OP comprises more  
 CC than 1 adjoined PSA-OP which generates a prostate specific response in  
 CC a portion of the human population. The PSA-OP can be used to produce  
 CC PSA specific cytotoxic T lymphocytes, in vivo or in vitro, which can  
 CC kill or prevent the establishment or growth of PSA positive tumour  
 CC cells, i.e. to prevent or treat prostatic cancer. The products may be  
 CC used to elicit a PSA specific immune response. When a recombinant virus  
 CC is used to elicit the response it is administered with a carrier, a  
 CC biological response modifier e.g. interleukin 2, 6 or 12, interferon,  
 CC tumour necrosis factor, granulocyte/macrophage-colony stimulating factor  
 CC or cyclophosphamide and an adjuvant selected from Ribi Dextox, QS21,  
 CC alum and incomplete Freund's adjuvant. PSA-OP comprises multiple PSA  
 CC epitopes, allowing an immune response to PSA in a population of humans  
 CC having more than 1 HLA class I molecule type to be generated.  
 CC  
 SQ Sequence 90 BP; 23 A; 24 C; 19 G; 24 T; 0 other;  
 Query Match 100.0%; Score 27; DB 18; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 0.0064;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AACTTCAGTGTGTGACCTCATGTT 27  
 DB 16 AACTTCAGTGTGTGACCTCATGTT 42  
 RESULT 3  
 AAT90074 standard; cDNA; 246 BP.  
 ID AAT90074  
 AC AAT90074;  
 DT 14-APR-1998 (first entry)  
 XX  
 DE Prostate specific antigen oligo-epitope encoding DNA.  
 XX  
 KM Prostate specific antigen; PSA; epitope; vaccine; immune response;  
 KM Prostatic tumour cell; human leukocyte antigen; HLA; cytotoxic;  
 KM T lymphocyte; cancer; ds.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT misc\_difference 58..60  
 FT /\*tag- a  
 FT /transl\_except- (pos:58..60,aa:Cys)  
 XX  
 PD WO9735021-A2.  
 XX  
 PD 25-SEP-1997.  
 XX  
 PD 19-MAR-1997; 97WO-US04454.  
 XX  
 PD 20-MAR-1996; 96US-0618936.  
 XX  
 PA (USSH ) US SEC DEPT HEALTH.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Schlom J, Tsang K, Zaremba S;  
 XX  
 DR WPI: 1997-480226/44.  
 DR P-PSDB: AAW27387.  
 XX  
 PT Prostate specific antigen multiple epitope peptide - useful in  
 PT vaccine to produce immune response against prostate specific antigen  
 PT in prostatic tumour cell  
 XX  
 PS Claim 23; Page 67; 85pp: English.  
 XX  
 CC The present sequence encodes a prostate specific antigen oligo-epitope  
 CC peptide (PSA-OP) for use in a virus vector of the present invention. The  
 CC PSA-OP comprises more than 1 adjoined PSA-OP which generates a prostate  
 CC specific response in a portion of the human population. The PSA-OP can  
 CC be used to produce PSA specific cytotoxic T lymphocytes, in vivo or in  
 CC vitro, which can kill or prevent the establishment or growth of PSA

CC positive tumour cells, i.e. to prevent or treat prostatic cancer. The  
CC products may be used to elicit a PSA specific immune response. When a  
CC recombinant virus is used to elicit the response it is coadministered  
CC with a carrier, a biological response modifier e.g. interleukin 2, 6 or  
CC 12, interferon, tumour necrosis factor, granulocyte/macrophage-colony  
CC stimulating factor or cyclophosphamide and an adjuvant selected from  
CC RIBI Detox, QS21, alum and incomplete Freund's adjuvant. PSA-OP  
CC comprises multiple PSA epitopes, allowing an immune response to PSA in  
CC a population of humans having more than 1 HLA class I molecule type to  
CC be generated.  
XX  
SQ Sequence 246 BP; 56 A; 51 C; 57 G; 82 T; 0 other;  
  
Query Match 100.0%; Score 27; DB 18; Length 246;  
Best Local Similarity 100.0%; Pred. No. 0.0076;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
Db 150 AAACCTCAGTGTGTGACCTCCATGTT 176  
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RESULT 4  
ID ABV38513 standard; cDNA; 420 BP.  
XX  
AC ABV38513;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 38504.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
PS  
XX Claim 1; Page 7841-7842; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (i) assessing the prostate cell carcinogenic potential of a compound;  
XX

CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 420 BP; 94 A; 127 C; 115 G; 84 T; 0 other;  
  
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Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
Db 362 AAACCTCAGTGTGTGACCTCCATGTT 388  
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ID ABV14332 standard; cDNA; 429 BP.  
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AC ABV14332;  
XX  
DT 13-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 14323.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
PS  
XX Claim 1; Page 2391; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 429 BP; 95 A; 122 C; 121 G; 91 T; 0 other;  
XX

Query Match 100.0%; Score 27; DB 23; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.0084;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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231 AAACCTCAGTGTGTGACCTCCATGTT 205

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AC ABV44545;  
XX  
DT 16-SEP-2002 (first entry)  
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DE Human prostate expression marker cDNA 44536.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
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PF 20-FEB-2001; 2001WO-US05171.  
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PR 17-FEB-2000; 2000US-183319P.  
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PR 16-MAR-2000; 2000US-189862P.  
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PR 25-MAY-2000; 2000US-207454P.  
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PR 09-JUN-2000; 2000US-211314P.  
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PR 18-JUL-2000; 2000US-219007P.  
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PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI: 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 8836; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 466 BP; 98 A; 140 C; 136 G; 92 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 466;  
Best Local Similarity 100.0%; Pred. No. 0.0086;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAACCTCAGTGTGTGACCTCCATGTT 27

DB 328 AAACCTCAGTGTGTGACCTCCATGTT 354  
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RESULT 7  
ABV35419/C  
ID ABV35419 standard; cDNA; 476 BP.  
XX  
AC ABV35419;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 35410.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
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PR 17-FEB-2000; 2000US-183319P.  
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PR 16-MAR-2000; 2000US-189862P.  
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PR 25-MAY-2000; 2000US-207454P.  
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PR 09-JUN-2000; 2000US-211314P.  
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PR 18-JUL-2000; 2000US-219007P.  
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PR 13-DEC-2000; 2000US-255281P.  
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PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI: 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX prostate cells and correlating with presence of prostate cancer, useful  
XX for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 7378; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
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RESULT 8  
ABV07463/C

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AC ABV07463:  
XX  
DT 13-SEP-2002 (first entry)  
XX  
XX Human prostate expression marker cDNA 7454.  
DE  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
OS  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
DR  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 1204-1205; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 492 BP; 102 A; 141 C; 115 G; 134 T; 0 other;  
XX  
QY Query Match 100.0%; Score 27; DB 23; Length 492;  
Best Local Similarity 100.0%; Pred. No. 0.0086;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 245 AAACCTCAGTGTGGACCTCCATGTT 27  
1 AAACCTCAGTGTGGACCTCCATGTT 27  
|||||  
16-SEP-2002 (first entry)  
XX  
XX RESULT 9  
ABV44248  
ID ABV44248 standard; cDNA; 616 BP.  
XX  
XX AC ABV44248:  
XX  
XX DT 16-SEP-2002 (first entry)  
XX

DE Human prostate expression marker cDNA 44239.  
XX  
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
OS  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
XX WPI; 2001-662795/76.  
XX  
DR  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 8788; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 616 BP; 122 A; 176 C; 186 G; 132 T; 0 other;  
XX  
QY Query Match 100.0%; Score 27; DB 23; Length 616;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 252 AAACCTCAGTGTGGACCTCCATGTT 27  
1 AAACCTCAGTGTGGACCTCCATGTT 27  
|||||  
16-SEP-2002 (first entry)  
XX  
XX RESULT 10  
ABV37397/C  
ID ABV37397 standard; cDNA; 632 BP.  
XX  
XX AC ABV37397:  
XX  
XX DT 16-SEP-2002 (first entry)  
XX  
XX DE Human prostate expression marker cDNA 37388.  
XX  
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX OS Homo sapiens.

PN WO200160860-A2.  
PD 23-AUG-2001.  
PF 20-FEB-2001; 2001WO-US05171.  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 26-MAY-2000; 2000US-207454P.  
PR 06-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-253281P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
PT WPI; 2001-662795/76.  
PS Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer

Claim 1: Page 7678; 11750pp: English.

The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:  
(a) assessing whether a patient is afflicted with prostate cancer;  
(b) monitoring the progression of prostate cancer in a patient;  
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;  
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;  
(e) selecting a composition for inhibiting prostate cancer in a patient;  
(f) assessing the prostate cell carcinogenic potential of a compound;  
(g) determining whether prostate cancer has metastasized in a patient;  
(h) assessing the aggressiveness or indolence of prostate cancer in a patient.  
(1) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 632 BP; 130 A; 182 C; 160 G; 160 T; 0 other;

Query Match 100.0%; Score 27; DB 23; Length 632;  
Best Local Similarity 100.0%; Pred. No. 0.009;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AACCTCAGTGTGTGGACCTCCATGTT 27  
|||||  
326 AAATTTCAGTGTGTGGACCTCCATGTT 300

RESULT 11  
ID AAT92976 standard; CDNA; 639 BP.  
XX AAT92976;  
XX  
XX AAT92976; (first entry)  
DT 24-APR-1998  
DE cDNA for prostate specific antigen (Psa).  
XX  
XX  
KW Diagnosis: prostate cancer; prostate specific antigen; PSA;  
KW metastatic-prostate cancer; prostate cell; secondary tumour;  
KW home\_metalstatie anchoring; ss.  
OS Homo sapiens.  
XX  
XX WC9739139-Al.  
XX  
XX 23-OCT-1997

```

PF      16-APR-1997:    97WO-US06497.
XX
PR      16-APR-1996:    96US-0015765.
XX
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI      Robbins DJ;
XX
DR      WPI: 1997-526473/48.
XX
PT      Monitoring or diagnosis of prostate cancer - by detecting
XX      prostate-specific antigen mRNA using specific primers
XX
PS      Disclosure; Page 16; 25pp; English.
XX
CC      CDNA sequences AAT92974-77 encode the prostate specific antigen (PSA).
CC      The detection of PSA mRNA in peripheral blood is associated with
CC      metastatic prostate cancer. Detection of PSA mRNA in the bloodstream
CC      indicates that prostate cells are circulating in the blood and confirms
CC      diagnosis of cancer. Circulating prostate cells also indicate a risk of a
CC      secondary tumour or bone metastatic anchoring. Detection of the PSA mRNA
CC      after prostatectomy or radiotherapy indicates a risk that the prostate
CC      cancer has spread and that the surgery and radiotherapy was not
CC      effective. PCR primers AAT92971-73 were used for the monitoring and
CC      diagnosis of patients with prostate cancer. The method comprises the
CC      detection of PSA mRNA by reverse transcriptase polymerase chain reaction
CC      (RT-PCR).
XX
SQ      Sequence 639 BP; 133 A; 191 C; 185 G; 130 T; 0 other:
XX
Query Match          100.0%; Score 27; DB:18; Length 639;
Best Local Similarity 100.0%; Pred.No. 0.0091;
Matches   27; Conservative    0; Mismatches    0; Indels    0; Gaps    0
OY      1 AAACCTCAGTGTGTGACCGCTCCATGTT 27
        |||||||
DB      486 AAACCTCAGTGTGTGACCGCTCCATGTT 512

RESULT: 12
ABV22297
ID      ABV22297 standard; cDNA; 651 BP.
XX
XX      ABV22297;
XX
DT      13-SEP-2002 (first entry)
XX
DE      Human prostate expression marker CDNA 22288.
XX
KW      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
OS      Homo sapiens.
XX
NN      WO200160860-A2.
XX
XX      23-AUG-2001.
XX
PD      20-FEB-2001; 2001WO-US05171.
XX
PF      17-FEB-2000; 2000US-183319P.
PR      16-MAR-2000; 2000US-189682P.
PR      25-MAY-2000; 2000US-207454P.
PR      09-JUN-2000; 2000US-211314P.
PR      18-JUL-2000; 2000US-219007P.
PR      13-DEC-2000; 2000US-255281P.
XX
PA      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI      Schlegel R, Endege WO, Monahan JE;
XX
WPI: 2001-662795/76.

```



PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
PS Claim 1; Page 3854; 11750bp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 651 BP; 164 A; 171 C; 156 G; 160 T; 0 other;  
XX  
Query Match 100.0%; Score 27; DB 23; Length 651;  
Best Local Similarity 100.0%; Pred. NO. 0.0091;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 AACTTCAGTGTGTGACCTCCATGTT 27  
ID AACTTCAGTGTGTGACCTCCATGTT 275  
Db 249 AACTTCAGTGTGTGACCTCCATGTT 275  
XX  
RESULT 13  
ABV28130  
XX ID ABV28130 standard; CDNA; 651 BP.  
XX AC ABV28130;  
XX DT 16-SEP-2002 (first entry)  
XX DE Human prostate expression marker CDNA 28121.  
XX KW Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX KW pharmacogenomic marker; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200160860-A2.  
XX PD 23-AUG-2001.  
XX PF 20-FEB-2001; 2001WO-US05171.  
XX PR 17-FEB-2000; 2000US-183319P.  
XX PR 16-MAR-2000; 2000US-189862P.  
XX PR 25-MAY-2000; 2000US-207454P.  
XX PR 09-JUN-2000; 2000US-211314P.  
XX PR 18-JUL-2000; 2000US-219007P.  
XX PR 13-DEC-2000; 2000US-255281P.  
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX PI Schlegel R, Endege WO, Monahan JE;  
XX DR WPI; 2001-662795/76.  
XX PT Novel isolated nucleic acid molecule associated with cancerous state of  
XX PT prostate cells and correlating with presence of prostate cancer, useful  
XX PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX PS Claim 1; Page 5827; 11750bp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 651 BP; 164 A; 171 C; 156 G; 160 T; 0 other;  
XX  
Query Match 100.0%; Score 27; DB 23; Length 651;  
Best Local Similarity 100.0%; Pred. NO. 0.0091;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 1 AACTTCAGTGTGTGACCTCCATGTT 27  
ID AACTTCAGTGTGTGACCTCCATGTT 275  
Db 249 AACTTCAGTGTGTGACCTCCATGTT 275  
XX  
RESULT 14  
AAV08947  
XX ID AAV08947 standard; CDNA; 711 BP.  
XX AC AAV08947;  
XX DT 27-APR-1999 (first entry)  
XX DE Human prostate specific antigen (PSA) gene.  
XX KW Human kallikrein 2; hK2; breast cancer; diagnosis; detection;  
XX KW treatment; monitoring; prostate specific antigen; PSA; ds.  
XX OS Homo sapiens.  
XX PN WO9859073-A1.  
XX PD 30-DEC-1998.  
XX PF 19-JUN-1998; 98WO-US12840.  
XX PR 20-JUN-1997; 97US-0050963.  
XX PA (KLEE/) KLEE G G.  
XX PA (MAYO-) MAYO FOUNDATION.  
XX PA (TIND/) TINDALL D J.  
XX PA (YOUN/) YOUNG C Y F.  
XX PI Klee GG, Tindall DJ, Young CYF;  
XX DR WPI; 1999-105632/09.  
XX DR P-PSDB; AAW96187.  
XX PT Use of human kallikrein 2 - as a marker for developing products for  
XX PT the diagnosis, prognosis, monitoring and treatment of breast cancer  
XX PS Disclosure; Page 34-35; 67pp; English.  
XX CC Human kallikrein 2 (hK2) is expressed at elevated levels relative to  
XX CC the prostate cancer antigen, prostate specific antigen (PSA) by  
XX CC breast cancer cells when stimulated by androgens. Detecting levels

CC of hK2 may provide a simple diagnostic tool for detecting or  
CC determining breast cancer. Detecting hK2 is achieved by producing  
CC an hK2 DNA from hK2 RNA by reverse transcription. The hK2 DNA  
CC obtained is then amplified by PCR and detected using probes.  
CC Determination of breast cancer may also be determined by exposing  
CC the hK2 polypeptide to an agent which binds to it and then detecting  
CC the binary complex formed. The amount of complex formed correlates  
CC directly to the presence of breast cancer in the human individual.  
CC The methods can be used in the diagnosis, treatment and/or  
CC monitoring of the progression or remission of breast cancer and/or  
CC monitoring hK2 levels.

XX  
SQ Sequence 711 BP; 148 A; 208 C; 206 G; 149 T; 0 other;

Query Match 100.0%; Score 27; DB 20; Length 711;

Best Local Similarity 100.0%; Pred. No. 0.0092;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
DB 436 AAACCTCAGTGTGTGACCTCCATGTT 462

RESULT 15

ABK86205  
ID ABK86205 standard; cDNA; 744 BP.

XX  
AC ABK86205;

XX  
DT 24-SEP-2002 (first entry)

XX  
DE cDNA encoding human prostate specific antigen (PSA) variant.

XX  
KW Human; prostate specific antigen; PSA; cytostatic; antiviral;

XX  
KW Immunostimulant; cell-mediated immune response; tumour; breast cancer;

XX  
KW Virus infection; prostate cancer; colorectal cancer; pancreatic cancer;

XX  
KW lymphoma; leukaemia; hepatitis; lentivirus; herpesvirus;

XX  
KW human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.

XX  
OS Homo sapiens.

XX  
FH Key

XX  
FH CDS

XX  
PD 23-MAY-2002.

XX  
PF 01-NOV-2001; 2001MO-US45626.

XX  
PR 01-NOV-2000; 2000US-0704232.

XX  
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.

XX  
PA (MINC/) MINCHEFF M S.

XX  
PA (LOUK/) LOUKINOV D I.

XX  
PA (ZOUB/) ZOUBAK S.

XX  
PI Mincheff MS, Loukinov DI, Zoubak S;

XX  
DR WPI: 2002-527524/56.

XX  
DR P-PSDB: AA098921.

XX  
PT Inducing a cell-mediated immune response against a target antigen,  
XX reducing undesired cells and stimulating presentation of an antigen by  
XX a cell, comprises administering a polynucleotide encoding a variant of  
XX an antigen -

XX  
PS Disclosure; Page 121-122; 146pp; English.

XX  
CC The invention relates to a method of inducing a cell-mediated immune

CC response against a cell comprising a target antigen (I) in a subject,  
CC treating a subject having undesired cells, for example tumour cells  
CC or virally infected cells (C), reducing the number of (C) in a subject,  
CC and stimulating presentation of (I) by a cell. This is done by  
CC administering a polynucleotide (II) encoding a variant of (I), so that  
CC (II) expressed in a cell and cell-mediated immune response is induced.  
CC The method can be used to treat prostate cancer, breast cancer,  
CC colorectal cancer and pancreatic cancer, as well as lymphomas and  
CC leukaemias. The method is also useful in treating chronic viral  
CC infections such as those caused by hepatitis, lentiviruses  
CC (including human immunodeficiency virus (HIV)), herpesviruses and the  
CC sequence of human prostate specific antigen (PSA) variant which  
CC has the signal sequence deleted, used as a target antigen in the method  
CC of the invention.

XX  
SQ Sequence 744 BP; 153 A; 222 C; 213 G; 156 T; 0 other;

Query Match 100.0%; Score 27; DB 24; Length 744;

Best Local Similarity 100.0%; Pred. No. 0.0093;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
DB 466 AAACCTCAGTGTGTGACCTCCATGTT 492

Search completed: November 19, 2002, 03:06:38  
Job time : 191.769 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 01:44:24 ; Search time 52.9615 Seconds  
(without alignments)  
156.345 Million cell updates/sec

Title: US-09-829-004A-9

Perfect score: 27  
Sequence: 1 aaacttcagtggtgacccatcatgtt 27

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapept 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/2/1na/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/PCRTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

#### SUMMARIES :

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	711	4	US-09-100-264-4
2	27	100.0	992	1	US-08-358-782D-13
3	27	100.0	992	2	US-08-764-527A-13
4	27	100.0	1350	4	US-09-605-785-616
5	27	100.0	1462	1	US-08-358-782D-14
6	27	100.0	1462	2	US-08-764-527A-14
7	27	100.0	1729	2	US-08-844-024-1
8	27	100.0	1729	2	US-08-844-024-1
9	27	100.0	7130	4	US-09-056-105-31
10	27	74.1	20	1	US-08-294-611-1
11	20	74.1	20	1	US-08-358-782D-1
12	20	74.1	20	1	US-08-586-993-1
13	20	74.1	20	1	US-08-764-527A-1
14	18.2	67.4	711	3	US-08-622-046B-2
15	18.2	67.4	711	3	US-08-622-046B-13
16	18.2	67.4	711	4	US-09-100-264-2
17	18.2	67.4	760	3	US-08-767-820A-7
18	18.2	67.4	760	3	US-08-767-820A-7
19	18.2	67.4	760	5	PCT-US95-06157-7
20	18.2	67.4	766	3	US-08-768-859A-9
21	18.2	67.4	766	3	US-08-767-820A-9
22	18.2	67.4	766	3	US-08-622-046B-6
23	18.2	67.4	766	3	US-08-622-046B-17
24	18.2	67.4	766	4	US-09-100-264-6
25	18.2	67.4	766	5	PCT-US95-06157-9
26	18.2	67.4	822	4	US-09-100-264-8
27	18.2	67.4	832	3	US-08-768-859A-5

28	18.2	67.4	832	3	US-08-768-859A-20	Sequence 20, Appl
29	18.2	67.4	832	3	US-08-767-820A-5	Sequence 5, Appl
30	18.2	67.4	832	3	US-08-767-820A-20	Sequence 20, Appl
31	18.2	67.4	832	3	US-08-622-046B-4	Sequence 4, Appl
32	18.2	67.4	832	3	US-08-622-046B-15	Sequence 15, Appl
33	18.2	67.4	832	5	PCT-US95-06157-5	Sequence 5, Appl
34	18.2	67.4	1341	4	US-08-983-075D-6	Sequence 6, Appl
35	18.2	67.4	1358	4	US-08-983-075D-8	Sequence 8, Appl
36	18.2	67.4	2417	4	US-09-439-313-334	Sequence 334, App
37	18.2	67.4	2417	4	US-09-352-616A-334	Sequence 334, App
38	18.2	67.4	2417	4	US-09-232-149A-334	Sequence 334, App
39	18.2	67.4	3674	4	US-09-605-785-698	Sequence 698, App
40	18.2	67.4	3360	1	US-08-408-093-5	Sequence 5, Appl
41	18	66.7	3360	1	US-08-408-093-5	Sequence 5, Appl
42	18	66.7	3360	1	US-08-714-901-5	Sequence 5, Appl
43	18	66.7	3360	3	US-08-040-741-5	Sequence 5, Appl
44	18	66.7	1548	4	US-09-099-053-1	Sequence 1, Appl
45	17.2	63.7				

#### ALIGNMENTS

```
RESULT 1
US-09-100-264-4
; Sequence 4, Application US/09100264
; Patent No. 6235486
; GENERAL INFORMATION:
; APPLICANT: Young, Charles Y.F.
; APPLICANT: Tindall, Donald J.
; APPLICANT: Klee, George G.
; TITLE OF INVENTION: Method for detection of breast cancer
; FILE REFERENCE: 545.006US1
; CURRENT APPLICATION NUMBER: US/09/100.264
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 60/050.963
; EARLIER FILING DATE: 1997-06-20
; NUMBER OF SEQ. ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-100-264-4

Query Match      100.0%; Score 27; DB 4; Length 711;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGGACCCATCATGTT 27
Db 436 AAACCTCAGTGTGGACCCATCATGTT 462

RESULT 2
US-08-358-782D-13
; Sequence 13, Application US/08358782D
; Patent No. 5674682
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Gomella, Leonard
; APPLICANT: Mulholland, S. Grant
; APPLICANT: Moreno, Jose
; APPLICANT: Fischer, Rainer
; TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th. Floor
; CITY: Philadelphia
; STATE: PA
; ZIP: 19103
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782D  
FILING DATE: 15-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 992 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-358-782D-13

Query Match 100.0%; Score 27; DB 1; Length 992;  
Best local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
|||||  
Db 551 AAACCTCAGTGTGTGACCTCCATGTT 577

## RESULT 3

US-08-764-527A-13  
Sequence 13, Application US/08764527A  
Patent No. 5938258  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo  
APPLICANT: Gonnella, Leonard  
APPLICANT: Mulholland, S. Grant  
APPLICANT: Moreno, Jose  
TITLE OF INVENTION: Methods of Detecting Micrometastasis of  
TITLE OF INVENTION: Prostate  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th. Floor  
CITY: Philadelphia  
STATE: PA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,527A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782  
FILING DATE: 15-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 992 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-764-527A-13

Query Match 100.0%; Score 27; DB 2; Length 992;  
Best local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
|||||  
Db 551 AAACCTCAGTGTGTGACCTCCATGTT 577

## RESULT 4

US-09-605-785-616  
Sequence 616, Application US/09605785  
Patent No. 6321716  
GENERAL INFORMATION:  
APPLICANT: Xu, Jidongchun  
APPLICANT: Dillon, David C.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqul  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedrick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Usaf A.W.  
TITLE OF INVENTION: REPER, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C16  
CURRENT APPLICATION NUMBER: US/09/605,785  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 616  
LENGTH: 1350  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-605-785-616

Query Match 100.0%; Score 27; DB 4; Length 1350;  
Best local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
|||||  
Db 1129 AAACCTCAGTGTGTGACCTCCATGTT 1155

## RESULT 5

US-08-358-782D-14  
Sequence 14, Application US/08358782D  
Patent No. 5674682  
GENERAL INFORMATION:  
APPLICANT: Croce, Carlo  
APPLICANT: Gonnella, Leonard  
APPLICANT: Mulholland, S. Grant  
APPLICANT: Moreno, Jose

APPLICANT: Fischer, Rainer  
TITLE OF INVENTION: Methods of Detecting Micrometastasis of Prostate  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th. Floor  
CITY: Philadelphia  
STATE: PA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782D  
FILING DATE: 15-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ. ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-358-782D-14

Query Match 100.0%; Score 27; DB 1; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGGACCTCCATGTT 27  
DB 532 AACTTCAGTGTGGACCTCCATGTT 558

RESULT 6  
US-08-764-527A-14  
Sequence 14, Application US/08764527A  
Patent No. 5939258  
GENERAL INFORMATION:  
APPLICANT: Crocker, Carlo  
APPLICANT: Gemella, Leonard  
APPLICANT: Mulholland, S. Grant  
APPLICANT: Moreno, Jose  
APPLICANT: Fischer, Rainer  
TITLE OF INVENTION: Methods of Detecting Micrometastasis of  
TITLE OF INVENTION: Prostate  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th. Floor  
CITY: Philadelphia  
STATE: PA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,527A  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782  
FILING DATE: 15-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell, Lori Y.  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-1327  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ. ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1462 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-764-527A-14

Query Match 100.0%; Score 27; DB 2; Length 1462;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCAGTGTGGACCTCCATGTT 27  
DB 532 AACTTCAGTGTGGACCTCCATGTT 558

RESULT 7  
US-08-844-024-1  
Sequence 1, Application US/08844024  
Patent No. 5840494  
GENERAL INFORMATION:  
APPLICANT: Katz, Aaron E., et al.  
TITLE OF INVENTION: A Method For Molecular Staging Of  
TITLE OF INVENTION: Prostate Cancer  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/844,024  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/229,391  
FILING DATE: 15-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 43677/JPW/TEP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 977-9550  
TELEFAX: (212) 664-0525  
TELEX: 422523 COOP UI  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1729 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA

Tue Nov 19 15:43:56 2002

us-09-829-004a-9.rml

Page 4

ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 378..1088  
US-08-844-024-1

Query Match  
Best Local Similarity 100.0%; Score 27; DB 2; Length 1729;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
DB 813 AAACCTCAGTGTGTGACCTCCATGTT 839

RESULT 8  
US-08-718-547-1  
Sequence 1, Application US/08718547  
Patent No. 5976794

GENERAL INFORMATION:  
APPLICANT: Katz, Aaron E.; Buttyan, Ralph; Raffo, Anthony;  
APPLICANT: Olsson, Carl A.  
TITLE OF INVENTION: A Method For Molecular Staging Of  
TITLE OF INVENTION: Prostate Cancer  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/718,547  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 43677-A-PCT/JPM/MJG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525

TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1729 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 378..1088  
US-08-718-547-1

Query Match  
Best Local Similarity 100.0%; Score 27; DB 2; Length 1729;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
DB 813 AAACCTCAGTGTGTGACCTCCATGTT 839

RESULT 9  
US-09-056-105-31  
Sequence 31, Application US/09056105  
Patent No. 6287569  
GENERAL INFORMATION:  
APPLICANT: KIPPS, THOMAS J.  
APPLICANT: MU, TONOI  
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
TITLE OF INVENTION: PROCESSING  
FILE REFERENCE: 233/221  
CURRENT APPLICATION NUMBER: US/09/056,105  
CURRENT FILING DATE: 1998-04-06  
EARLIER APPLICATION NUMBER: 60/043,467  
EARLIER FILING DATE: 1997-04-10  
SOFTWARE: FastSeq for Windows Version 3.0  
NUMBER OF SEQ ID NOS: 35  
SEQ ID NO 31  
LENGTH: 7130  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-056-105-31

Query Match

Best Local Similarity 100.0%; Score 27; DB 4; Length 7130;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAACCTCAGTGTGTGACCTCCATGTT 27  
DB 4200 AAACCTCAGTGTGTGACCTCCATGTT 4226

RESULT 10  
US-08-294-611-1/C  
Sequence 1, Application US/08294611  
Patent No. 5506106  
GENERAL INFORMATION:  
APPLICANT: Croce et al.  
TITLE OF INVENTION: Methods of Detecting  
TITLE OF INVENTION: Micrometastasis Of Prostate Cancer  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/294,611  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/973,322  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lori Y. Beardsell  
REGISTRATION NUMBER: 34,293  
REFERENCE/DOCKET NUMBER: TJU-0722  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic  
STRANDEDNESS: Single  
TOPOLOGY: Linear



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,527A  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,782  
FILING DATE: 15-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Beardell J. Scott 3,  
REGISTRATION NUMBER: 34,293  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3439  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-764-527A-1

Query Match  
Best Local Similarity 74.1%; Score 20; DB 2; Length 20;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 AACCTCAGTGTGTGACCTC 21  
20 AACCTCAGTGTGTGACCTC 1

RESULT 14  
US-08-622-046B-2  
Sequence 2, Application US/08622046B  
Patent No. 6103237  
GENERAL INFORMATION:  
APPLICANT: Saeedi, Mohammed S.  
TITLE OF INVENTION: Stable Variant HK2 Polypeptide  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/622,046B  
FILING DATE: 26-MARCH-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.  
REGISTRATION NUMBER: 30,440  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-373-6903  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:

LENGTH: 711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-622-046B-2

Query Match  
Best Local Similarity 67.4%; Score 18.2; DB 3; Length 711;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 439 CTTACAGTGTGTGACCTCATCT 461  
4 CTTACAGTGTGTGACCTCATCT 26

RESULT 15  
US-08-622-046B-13  
Sequence 13, Application US/08622046B  
Patent No. 6103237  
GENERAL INFORMATION:  
APPLICANT: Saeedi, Mohammed S.  
TITLE OF INVENTION: Stable Variant HK2 Polypeptide  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Schweigman, Lundberg, Woessner & Kluth, P.A.  
STREET: P.O. Box 2938  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/622,046B  
FILING DATE: 26-MARCH-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Woessner, Warren D.  
REGISTRATION NUMBER: 30,440  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-373-6903  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-622-046B-13

Query Match  
Best Local Similarity 67.4%; Score 18.2; DB 3; Length 711;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 439 CTTACAGTGTGTGACCTCATCT 461  
4 CTTACAGTGTGTGACCTCATCT 26

Search completed: November 19, 2002, 05:20:22  
Job time : 53.9615 secs